

DT05 Rec'd PCT/PTO 17 FEB 2005

SEQUENCE LISTING

5 <110> SunGene GmbH Co. KGaA

<120> Use of astaxanthin-containing plants or parts of plants of the ge-
10 nus Tagetes as feedstuffs

<130> PF 54148
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<160> 142
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<170> PatentIn version 3.1

25 <210> 1

<211> 1771

30 <212> DNA

<213> Haematococcus pluvialis

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<221> CDS

40 <222> (166)..(1155)

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BEST AVAILABLE COPY

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Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
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Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
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Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
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His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
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Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
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20	Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala	100	105	110	
25	Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr	115	120	125	
30	Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu	130	135	140	
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40	Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly	165	170	175	
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Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
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Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
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 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
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 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
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Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
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Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
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Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
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Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212

Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp

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Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
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Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45
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Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60
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His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80
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Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95
 30

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110
 35

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125
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Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140
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Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160
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Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
 165 170 175

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Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
 180 185 190

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Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205

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Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
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Arg Ala

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atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
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gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

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aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
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cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

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gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg 288
 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

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cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc 336
 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

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gac gac gac cca gat ttc gac cat gcc ggc ccg gtc cgc tgg tac gcc 384
 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

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cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc 432
 Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

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gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac 480
 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

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gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc 528
 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg 576
 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

21

gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg 624
 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

5 ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac 672
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

10 ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
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 Thr Ala

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 35 40 45

40

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
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45

22

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

5 Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

10 Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

15 Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

20 Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

25 Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

30 Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

35 Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

40 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
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Thr Ala

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 gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta 96
 30 Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
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 gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg 144
 Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
 35 35 40 45
 ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac 192
 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60
 40 gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag 240
 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80
 45 tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg 288

	Tyr	Gly	Leu	Glu	Tyr	Leu	Phe	Cys	Asp	Pro	Ser	Val	Phe	Cys	Pro	Gly	
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5	ctg	gat	ggc	caa	gct	ttt	atg	agc	tac	cgt	tcc	cta	gaa	aaa	acc	tgt	336
	Leu	Asp	Gly	Gln	Ala	Phe	Met	Ser	Tyr	Arg	Ser	Leu	Glu	Lys	Thr	Cys	
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10	gcc	cac	att	gcc	acc	tat	agc	ccc	cga	gat	gcg	gaa	aaa	tat	cgg	caa	384
	Ala	His	Ile	Ala	Thr	Tyr	Ser	Pro	Arg	Asp	Ala	Glu	Lys	Tyr	Arg	Gln	
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15	ttt	gtc	aat	tat	tgg	acg	gat	ttg	ctc	aac	gct	gtc	cag	cct	gct	ttt	432
	Phe	Val	Asn	Tyr	Trp	Thr	Asp	Leu	Leu	Asn	Ala	Val	Gln	Pro	Ala	Phe	
		130					135				140						
	aat	gct	ccg	ccc	cag	gct	tta	cta	gat	tta	gcc	ctg	aac	tat	ggg	tgg	480
	Asn	Ala	Pro	Pro	Gln	Ala	Leu	Leu	Asp	Leu	Ala	Leu	Asn	Tyr	Gly	Trp	
	145				150					155					160		
20	gaa	aac	tta	aaa	tcc	gtg	ctg	gcg	atc	gcc	ggg	tcg	aaa	acc	aag	gcg	528
	Glu	Asn	Leu	Lys	Ser	Val	Leu	Ala	Ile	Ala	Gly	Ser	Lys	Thr	Lys	Ala	
				165					170					175			
25	ttg	gat	ttt	atc	cgc	act	atg	atc	ggc	tcc	ccg	gaa	gat	gtg	ctc	aat	576
	Leu	Asp	Phe	Ile	Arg	Thr	Met	Ile	Gly	Ser	Pro	Glu	Asp	Val	Leu	Asn	
				180					185					190			
30	gaa	tgg	ttc	gac	agc	gaa	cgg	gtt	aaa	gct	cct	tta	gct	aga	cta	tgt	624
	Glu	Trp	Phe	Asp	Ser	Glu	Arg	Val	Lys	Ala	Pro	Leu	Ala	Arg	Leu	Cys	
		195					200						205				
35	tcg	gaa	att	ggc	gct	ccc	cca	tcc	caa	aag	ggg	agt	agc	tcc	ggc	atg	672
	Ser	Glu	Ile	Gly	Ala	Pro	Pro	Ser	Gln	Lys	Gly	Ser	Ser	Ser	Gly	Met	
		210					215					220					
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	Met	Met	Val	Ala	Met	Arg	His	Leu	Glu	Gly	Ile	Ala	Arg	Pro	Lys	Gly	
	225				230				235					240			
40	ggc	act	gga	gcc	ctc	aca	gaa	gcc	ttg	gtg	aag	tta	gtg	caa	gcc	caa	768
	Gly	Thr	Gly	Ala	Leu	Thr	Glu	Ala	Leu	Val	Lys	Leu	Val	Gln	Ala	Gln	
				245					250					255			
45	ggg	gga	aaa	atc	ctc	act	gac	caa	acc	gtc	aaa	cgg	gta	ttg	gtg	gaa	816
	Gly	Gly	Lys	Ile	Leu	Thr	Asp	Gln	Thr	Val	Lys	Arg	Val	Leu	Val	Glu	

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	260	265	270	
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	Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg			
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	gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg			912
	Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu			
	290	295	300	
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	caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg			960
	Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly			
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	gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa			1008
	Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys			
	325	330	335	
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	atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg			1056
	Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly			
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	ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat			1104
	Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His			
	355	360	365	
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	gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct			1152
	Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala			
	370	375	380	
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	aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg			1200
	Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met			
	385	390	395	400
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	gcc ccc cct ggg cag cac acc ctc tgg atc gaa ttt ttt gcc ccc tac			1248
	Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr			
	405	410	415	
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	cgc atc gcc ggg ttg gaa ggg aca ggg tta atg ggc aca ggt tgg acc			1296
	Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr			
	420	425	430	
	gat gag tta aag gaa aaa gtg gcg gat cgg gtg att gat aaa tta acg			1344
	Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr			
	435	440	445	

gac tat gcc cct aac cta aaa tct ctg atc att ggt cgc cga gtg gaa 1392
 Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
 450 455 460

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agt ccc gcc gaa ctg gcc caa cgg ctg gga agt tac aac ggc aat gtc 1440
 Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
 465 470 475 480

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tat cat ctg gat atg agt ttg gac caa atg atg ttc ctc cgg cct cta 1488
 Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
 485 490 495

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ccg gaa att gcc aac tac caa acc ccc atc aaa aat ctt tac tta aca 1536
 Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

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ggg gcg ggt acc cat ccc ggt ggc tcc ata tca ggt atg ccc ggt aga 1584
 Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

25

aat tgc gct cgg gtc ttt tta aaa caa caa cgt cgt ttt tgg taa 1629
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Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
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5 Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
 50 55 60

10 Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
 65 70 75 80

15 Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
 85 90 95

20 Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
 100 105 110

Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
 115 120 125

25 Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
 130 135 140

30 Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
 145 150 155 160

35 Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala
 165 170 175

40 Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn
 180 185 190

Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys
 195 200 205

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28

Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met
 210, 215 220

5 Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly
 225 230 235 240

10 Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln
 245 250 255

15 Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu
 260 265 270

Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg
 275 280 285

20 Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu
 290 295 300

25 Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly
 305 310 315 320

30 Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys
 325 330 335

35 Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly
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Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His
 355 360 365

40 Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala
 370 375 380

45 Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met

385 390 395 400

Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr
5 405 410 415

Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr
10 420 425 430

Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr
15 435 440 445

Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu
20 450 455 460

Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val
25 465 470 475 480

Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu
25 485 490 495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
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Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
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Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
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<213> Bradyrhizobium sp.

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 Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
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25 atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144
 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

30 ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
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acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240
 Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80

35 ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288
 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95

40 ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336
 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110

45 gag cac cac aag cat cac cgc cat ccc ggc acg gcc gag gat ccc gat 384
 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp

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	Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe			
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	Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val			
	145	150	155	160
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	Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu			
	165	170	175	
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15	Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr			
	180	185	190	
	ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat			624
20	Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp			
	195	200	205	
	cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tgc ctg ctg			672
	Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu			
25	210	215	220	
	acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat			720
	Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp			
	225	230	235	240
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Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
35 40 45

20

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
50 55 60

25

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
85 90 95

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Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
100 105 110

35

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
115 120 125

40

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
130 135 140

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Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
165 170 175

5
Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

10
Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
195 200 205

15
Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

20
Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
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10 ttg tca tcg aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
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15 att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

20 ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

25 atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat 288
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

30 ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

35 gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat 384
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

40 tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

45 tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480
 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

35

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	Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu	
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	Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val	
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10	caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt	624
	Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly	
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15	ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt	672
	Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe	
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	Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His	
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	gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata	768
	Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile	
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Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

5 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

10 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

15 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

20 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

25 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

30 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

35 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

40 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

45 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly

195

200

205

5 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
210 215 220

10 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
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Ser Leu

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Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
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47

45 ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg

95

38

	Gly	Pro	Pro	Pro	His	Leu	His	Arg	Ser	Phe	Ala	Ala	Thr	Thr	Met	Leu	
					20					25					30		
	tcg	aag	ctg	cag	tca	atc	agc	gtc	aag	gcc	cgc	cgc	gtt	gaa	cta	gcc	143
5	Ser	Lys	Leu	Gln	Ser	Ile	Ser	Val	Lys	Ala	Arg	Arg	Val	Glu	Leu	Ala	
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	cgc	gac	atc	acg	cgg	ccc	aaa	gtc	tgc	ctg	cat	gct	cag	cgg	tgc	tcg	191
10	Arg	Asp	Ile	Thr	Arg	Pro	Lys	Val	Cys	Leu	His	Ala	Gln	Arg	Cys	Ser	
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	Leu	Val	Arg	Leu	Arg	Val	Ala	Ala	Pro	Gln	Thr	Glu	Glu	Ala	Leu	Gly	
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	Thr	Val	Gln	Ala	Ala	Gly	Ala	Gly	Asp	Glu	His	Ser	Ala	Asp	Val	Ala	
	80					85				90				95			
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	Leu	Gln	Gln	Leu	Asp	Arg	Ala	Ile	Ala	Glu	Arg	Arg	Ala	Arg	Arg	Lys	
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25	Arg	Glu	Gln	Leu	Ser	Tyr	Gln	Ala	Ala	Ala	Ile	Ala	Ala	Ser	Ile	Gly	
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	Met	Thr	Val	Gly	Gly	Ala	Val	Pro	Trp	Gly	Glu	Val	Ala	Gly	Thr	Leu	
		145				150					155						
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	Leu	Leu	Val	Val	Gly	Gly	Ala	Leu	Gly	Met	Glu	Met	Tyr	Ala	Arg	Tyr	
	160					165				170				175			
40	gca	cac	aaa	gcc	atc	tgg	cat	gag	tcg	cct	ctg	ggc	tgg	ctg	ctg	cac	575
	Ala	His	Lys	Ala	Ile	Trp	His	Glu	Ser	Pro	Leu	Gly	Trp	Leu	Leu	His	
				180				185					190				
	aag	agc	cac	cac	aca	cct	cgc	act	gga	ccc	ttt	gaa	gcc	aac	gac	ttg	623
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5 ggctcgtgcc agaaatggtg agtggatgac tgtgacgctg tacattgcag gcaggtgaga 1551

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35 40 45

35 Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu

50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr

40 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu

85 90 95

45

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
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5

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
 115 120 125

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Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
 130 135 140

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Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
 145 150 155 160

20

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
 165 170 175

25

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
 195 200 205

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Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
 210 215 220

35

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
 225 230 235 240

40

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
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His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

45

42

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

5 Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
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Lys Arg

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1 5 10 15

cat cat ggt ttt gct gtt aaa gct agt acc ttt aga tct gag aag cat 96

His His Gly Phe Ala Val Lys Ala Ser Thr Phe Arg Ser Glu Lys His

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45

	cat aat ttt ggt tct agg aag ttt tgt gaa act ttg ggt aga agt gtt	144
	His Asn, Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val	
	35 40 45	
5	tgt gtt aag ggt agt agt agt gct ctt tta gag ctt gta cct gag acc	192
	Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr	
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10	aaa aag gag aat ctt gat ttt gag ctt cct atg tat gac cct tca aaa	240
	Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys	
	65 70 75 80	
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	Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu	
	85 90 95	
20	gct gtt gca cag caa gtt tct gaa gca gga ctc tct gtt tgt tca att	336
	Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile	
	100 105 110	
25	gat ccg aat cct aaa ttg ata tgg cct aat aac tat ggt gtt tgg gtg	384
	Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val	
	115 120 125	
30	gat gaa ttt gag gct atg gac ttg tta gat tgt cta gat gct acc tgg	432
	Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp	
	130 135 140	
35	tct ggt gca gca gtg tac att gat gat aat acg gct aaa gat ctt cat	480
	Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His	
	145 150 155 160	
40	aga cct, tat gga agg gtt aac cgg aaa cag ctg aaa tcg aaa atg atg	528
	Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met	
	165 170 175	
45	cag aaa tgt ata atg aat ggt gtt aaa ttc cac caa gcc aaa gtt ata	576
	Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile	
	180 185 190	
50	aag gtg att cat gag gaa tcg aaa tcc atg ttg ata tgc aat gat ggt	624
	Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly	
	195 200 205	
55	att act att cag gca acg gtg gtg ctc gat gca act ggc ttc tct aga	672

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	225 230 235 240	
10	tat ggc att ttg gct gaa gtg gaa gag cac ccc ttt gat gta aac aag Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys	768
	245 250 255	
15	atg gtt ttc atg gat tgg cga gat tct cat ttg aag aac aat act gat Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp	816
	260 265 270	
	ctc aag gag aga aat agt aga ata cca act ttt ctt tat gca atg cca Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro	864
	275 280 285	
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	290 295 300	
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	305 310 315 320	
30	aac cat ttg ggg ata aaa gtg aag agc att gaa gaa gat gaa cat tgt Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys	1008
	325 330 335	
35	cta ata cca atg ggt ggt cca ctt cca gta tta cct cag aga gtc gtt Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val	1056
	340 345 350	
	gga atc ggt ggt aca gct ggc atg gtt cat cca tcc acc ggt tat atg Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met	1104
	355 360 365	
40	gtg gca agg aca cta gct gcg gct cct gtt gtt gcc aat gcc ata att Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile	1152
	370 375 380	
45	caa tac ctc ggt tct gaa aga agt cat tcg ggt aat gaa tta tcc aca Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr	1200

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	Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala							
			420		425		430	
10	aca aga agg ttc ttt gat gca ttc ttt gac tta gaa cct cgt tat tgg							1344
	Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp							
			435		440		445	
15	cat ggc ttc tta tgc tct cga ttg ttt cta cct gaa ctc ata gtt ttt							1392
	His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe							
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	ggg ctg tct cta ttc tct cat gct tca aat act tct aga ttt gag ata							1440
20	Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile							
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	atg aca aag gga act gtt cca tta gta aat atg atc aac aat ttg tta							1488
	Met Thr Lys Gly Thr Val Pro Leu Val Asn Met Ile Asn Asn Leu Leu							
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10 His Asn Phe Gly Ser Arg Lys Phe Cys Glu Thr Leu Gly Arg Ser Val
 35 40 45

15 Cys Val Lys Gly Ser Ser Ser Ala Leu Leu Glu Leu Val Pro Glu Thr
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20 Lys Lys Glu Asn Leu Asp Phe Glu Leu Pro Met Tyr Asp Pro Ser Lys
 65 70 75 80

25 Gly Val Val Val Asp Leu Ala Val Val Gly Gly Gly Pro Ala Gly Leu
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30 Ala Val Ala Gln Gln Val Ser Glu Ala Gly Leu Ser Val Cys Ser Ile
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35 Asp Pro Asn Pro Lys Leu Ile Trp Pro Asn Asn Tyr Gly Val Trp Val
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40 Asp Glu Phe Glu Ala Met Asp Leu Leu Asp Cys Leu Asp Ala Thr Trp
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45 Ser Gly Ala Ala Val Tyr Ile Asp Asp Asn Thr Ala Lys Asp Leu His
 145 150 155 160

50 Arg Pro Tyr Gly Arg Val Asn Arg Lys Gln Leu Lys Ser Lys Met Met
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55 Gln Lys Cys Ile Met Asn Gly Val Lys Phe His Gln Ala Lys Val Ile
 180 185 190

Lys Val Ile His Glu Glu Ser Lys Ser Met Leu Ile Cys Asn Asp Gly
 195 200 205

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Ile Thr Ile Gln Ala Thr Val Val Leu Asp Ala Thr Gly Phe Ser Arg
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Ser Leu Val Gln Tyr Asp Lys Pro Tyr Asn Pro Gly Tyr Gln Val Ala
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Tyr Gly Ile Leu Ala Glu Val Glu Glu His Pro Phe Asp Val Asn Lys
 245 250 255

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Met Val Phe Met Asp Trp Arg Asp Ser His Leu Lys Asn Asn Thr Asp
 260 265 270

Leu Lys Glu Arg Asn Ser Arg Ile Pro Thr Phe Leu Tyr Ala Met Pro
 275 280 285

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Phe Ser Ser Asn Arg Ile Phe Leu Glu Glu Thr Ser Leu Val Ala Arg
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Pro Gly Leu Arg Ile Asp Asp Ile Gln Glu Arg Met Val Ala Arg Leu
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35

Asn His Leu Gly Ile Lys Val Lys Ser Ile Glu Glu Asp Glu His Cys
 325 330 335

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Leu Ile Pro Met Gly Gly Pro Leu Pro Val Leu Pro Gln Arg Val Val
 340 345 350

Gly Ile Gly Gly Thr Ala Gly Met Val His Pro Ser Thr Gly Tyr Met
 355 360 365

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Val Ala Arg Thr Leu Ala Ala Ala Pro Val Val Ala Asn Ala Ile Ile
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5 Gln Tyr Leu Gly Ser Glu Arg Ser His Ser Gly Asn Glu Leu Ser Thr
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10 Ala Val Trp Lys Asp Leu Trp Pro Ile Glu Arg Arg Arg Gln Arg Glu
 405 410 415

15 Phe Phe Cys Phe Gly Met Asp Ile Leu Leu Lys Leu Asp Leu Pro Ala
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Thr Arg Arg Phe Phe Asp Ala Phe Phe Asp Leu Glu Pro Arg Tyr Trp
 435 440 445

20 His Gly Phe Leu Ser Ser Arg Leu Phe Leu Pro Glu Leu Ile Val Phe
 450 455 460

25 Gly Leu Ser Leu Phe Ser His Ala Ser Asn Thr Ser Arg Phe Glu Ile
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	Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser				
		35	40	45	
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	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc				194
	Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser				
	50	55	60		
15					
	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gcc				242
	Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala				
	65	70	75		
	gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg				290
20	Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu				
	80	85	90	95	
	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt				338
	Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val				
25		100	105	110	
	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg				386
	Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu				
		115	120	125	
30					
	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat				434
	Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His				
	130	135	140		
35					
	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga				482
	Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg				
	145	150	155		
	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc				530
40	Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg				
	160	165	170	175	
	aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct				578
	Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro				
45		180	185	190	

5 bac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc 626
 Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe
 195 200 205

atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg 674
 Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp
 210 215 220

10 acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg 722
 Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val
 225 230 235

15 ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt 770
 Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe
 240 245 250 255

20 ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct 818
 Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser
 260 265 270

25 tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc 866
 Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser
 275 280 285

30 gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag 914
 Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu
 290 295 300

35 cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc 962
 His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg
 305 310 315

40 cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc 1015
 Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 320 325

cctgctgccca gctgggcatg cagggttgtgg caggactggg tgaggtgaaa agctgcaggc 1075

40 gctgctgccg gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg 1135

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5 <212> PRT

<213> Haematococcus pluvialis

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Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

25

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

30

Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

35

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

40

Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

45

Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly

130

135

140

5 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
145 150 155 160

10 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
165 170 175

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
180 185 190

15 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
195 200 205

20 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
210 215 220

25 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
225 230 235 240

30 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
245 250 255

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
260 265 270

35 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
275 280 285

40 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
290 295 300

45 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala

325

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<210> 24

<211> 1111

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<213> Haematococcus pluvialis

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<400> 24

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Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser

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10

15

tct gac gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gaa 96

Ser Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu

20

25

30

35

gag tca gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca 144

Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro

35

40

45

40

cct tcc gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc 192

Pro Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser

50

55

60

tgg gcc gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc 240

45

Trp Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr

	65	70	75	
	tcc ttg gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag			288
	Ser Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln			
5	80	85	90	95
	ctg gtt agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt			336
	Leu Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe			
	100	105	110	
10	gtc ctg gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct			384
	Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala			
	115	120	125	
15	atg cat ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg			432
	Met His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu			
	130	135	140	
	ggc aga gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg			480
20	Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu			
	145	150	155	
	cac cgc aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag			528
	His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys			
25	160	165	170	175
	gac cct gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc			576
	Asp Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala			
	180	185	190	
30	agc ttc atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca			624
	Ser Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala			
	195	200	205	
35	tgg tgg acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg			672
	Trp Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu			
	210	215	220	
	ctg gtg ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc			720
40	Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe			
	225	230	235	
	tac ttt ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca			768
	Tyr Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser			
45	240	245	250	255

ggc tct tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag 816
 Gly Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln
 260 265 270

5

gcg tcc gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac 864
 Ala Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His
 275 280 285

10

tgg gag cac cac cgc tgg ccc ttc gcc ccc tgg tgg gag ctg ccc aac 912
 Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn
 290 295 300

15

tgc cgc cgc ctg tct ggc cga ggt ctg gtt cct gcc tag ctggacacac 961
 Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 305 310 315

20

tgcagtgggc cctgctgccg gctgggcatg caggttgtgg caggactggg tgaggtgaaa 1021
 agctgcaggc gctgctgccg gacacgttgc atgggctacc ctgtgtagct gccgccacta 1081
 ggggaggggg tttgtagctg tcgagcttgc 1111

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<210> 25
 <211> 315
 <212> PRT

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<213> Haematococcus pluvialis

35

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 Met Leu Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser
 1 5 10 15

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Asp Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu
 20 25 30

45

Ser Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro

	35	40	45
5	Ser Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp		
	50	55	60
10	Ala Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser		
	65	70	75 80
15	Leu Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu		
	85	90	95
20	Val Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val		
	100	105	110
25	Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met		
	115	120	125
30	His Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly		
	130	135	140
35	Arg Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His		
	145	150	155 160
40	Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp		
	165	170	175
45	Pro Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser		
	180	185	190
50	Phe Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp		
	195	200	205
55	Trp Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu		
	210	215	220

Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr
 225 230 235 240

5

Phe Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly
 245 250 255

10

Ser Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala
 260 265 270

15

Ser Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp
 275 280 285

20

Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys
 290 295 300

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Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala
 305 310 315

<210> 26

<211> 1031

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<212> DNA

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10	gct gag gca ctc aag gag aag gag aag gag gtt gca ggc agc tct gac Ala Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp 20 25 30	98
15	gtg ttg cgt aca tgg gcg acc cag tac tcg ctt ccg tca gag gag tca Val Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser 35 40 45	146
	gac gcg gcc cgc ccg gga ctg aag aat gcc tac aag cca cca cct tcc Asp Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser 50 55 60	194
20	gac aca aag ggc atc aca atg gcg cta gct gtc atc ggc tcc tgg gct Asp Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala 65 70 75	242
25	gca gtg ttc ctc cac gcc att ttt caa atc aag ctt ccg acc tcc ttg Ala Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu 80 85 90 95	290
30	gac cag ctg cac tgg ctg ccc gtg tca gat gcc aca gct cag ctg gtt Asp Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val 100 105 110	338
35	agc ggc agc agc agc ctg ctg cac atc gtc gta gta ttc ttt gtc ctg Ser Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu 115 120 125	386
40	gag ttc ctg tac aca ggc ctt ttt atc acc acg cat gat gct atg cat Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His 130 135 140	434
	ggc acc atc gcc atg aga aac agg cag ctt aat gac ttc ttg ggc aga Gly Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg 145 150 155	482
45	gta tgc atc tcc ttg tac gcc tgg ttt gat tac aac atg ctg cac cgc Val Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg	530

160	165	170	175	
aag cat tgg gag cac cac aac cac act ggc gag gtg ggc aag gac cct				578
Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro				
5	180	185	190	
gac ttc cac agg gga aac cct ggc att gtg ccc tgg ttt gcc agc ttc				626
Asp Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe				
	195	200	205	
10				
atg tcc agc tac atg tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg				674
Met Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp				
	210	215	220	
15				
acg gtg gtc atg cag ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg				722
Thr Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val				
	225	230	235	
20				
ttc atg gcg gcc gcg ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt				770
Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe				
	240	245	250	255
25				
ggc acg tac atg ccc cac aag cct gag cct ggc gcc gcg tca ggc tct				818
Gly Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser				
	260	265	270	
30				
tca cca gcc gtc atg aac tgg tgg aag tcg cgc act agc cag gcg tcc				866
Ser Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser				
	275	280	285	
35				
gac ctg gtc agc ttt ctg acc tgc tac cac ttc gac ctg cac tgg gag				914
Asp Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu				
	290	295	300	
40				
cac cac cgc tgg ccc ttt gcc ccc tgg tgg gag ctg ccc aac tgc cgc				962
His His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg				
	305	310	315	
45				
cgc ctg tct ggc cga ggt ctg gtt cct gcc gag caa aaa ctc atc tca				1010
Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser				
	320	325	330	335
gaa gag gat ctg aat agc tag				1031
Glu Glu Asp Leu Asn Ser				
	340			

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 1 5 10 15
 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 20 25 30
 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 25 35 40 45
 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60
 30 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80
 35 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95
 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 40 100 105 110
 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125
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Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

5

Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

10

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

15

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

20

Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

25

Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

30

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

35

Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

40

Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

45

63

His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 '305 310 315 320

5 Leu Ser Gly Arg Gly Leu Val Pro Ala Glu Gln Lys Leu Ile Ser Glu
 325 330 335

10 Glu Asp Leu Asn Ser
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15 <211> 777

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20 <213> Arabidopsis thaliana

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agcaaaaaga aaaaagagtt tcatcatata tctgatttga tggactggtt ggagtttagga 180

40 ccaaacatta tctacaaaca aagacttttc tcttaacttg tgattccttc ttaaacccta 240

ggggtaatat tctattttcc aaggatcttt agttaaaggc aaatccggga aattattgta 300

45 atcatttggg gaaacatata aaagatttga gttagatgga agtgacgatt aatccaaaca 360

64

tatatatctc tttcttctta tttcccaaat taacagacaa aagtagaata ttggctttta 420
acaccaatat aaaaacttgc ttcacaccta aacacttttg tttacttttag ggtaagtgca 480
5 aaaagccaac caaatccacc tgcactgatt tgacgtttac aaacgccgtt aagtcgatgt 540
ccgttgattt aaacagtgtc ttgtaattaa aaaaatcagt ttacataaat ggaaaattta 600
tcacttagtt ttcacaaact tctgaactta cttttcatgg attaggcaat actttccatt 660
10 tttagtaact caagtggacc ctttacttct tcaactccat ctctctcttt ctatttcact 720
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gcaagctcga cagctacaaa cc 22
40 <210> 30
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5 <220>

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<210> 31

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<223>

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<210> 32

<211> 59

<212> DNA

5 <213> synthetic

<220>

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35

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5 <210> 34
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15 <222> (1)..(37)
<223>
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30 <212> DNA
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40 <222> (1)..(34)
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atcaacggac atcgacttaa cggcgtttgt aaac

34

5 <210> 36

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15 <220>

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35 <213> Synthetic sequence

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 gtagtaatat aatatttcaa atattttttt caaaataaaa gaatgtagta tatagcaatt 120
 gcttttctgt agtttataag tgtgtatatt ttaatttata actttttctaa tatatgacca 180
 10 aaatttggtg atgtgcaggt atcaccggat cc. 212

<210> 38
 15 <211> 1830
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 20 <213> Tagetes erecta

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 30 <223>

<400> 38
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 gatacaaggc gtgactggat atttctctct cgttcctaac aacagcaacg aagaagaaaa 120
 agaatcatta ctaacaatca atg agt atg aga gct gga cac atg acg gca aca 173
 40 Met Ser Met Arg Ala Gly His Met Thr Ala Thr
 1 5 10
 atg gcg gct ttt aca tgc cct agg ttt atg act agc atc aga tac acg 221
 Met Ala Ala Phe Thr Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr
 45 15 20 25

aag caa att aag tgc aac gct gct aaa agc cag cta gtc gtt aaa caa 269
 Lys Gln Ile Lys Cys Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln
 30 35 40

5

gag att gag gag gaa gaa gat tat gtg aaa gcc ggt gga tcg gag ctg 317
 Glu Ile Glu Glu Glu Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu
 45 50 55

10

ctt ttt gtt caa atg caa cag aat aag tcc atg gat gca cag tct agc 365
 Leu Phe Val Gln Met Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser
 60 65 70 75

15

cta tcc caa aag ctc cca agg gta cca ata gga gga gga gga gac agt 413
 Leu Ser Gln Lys Leu Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser
 80 85 90

20

aac tgt ata ctg gat ttg gtt gta att ggt tgt ggt cct gct ggc ctt 461
 Asn Cys Ile Leu Asp Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu
 95 100 105

25

gct ctt gct gga gaa tca gcc aag cta ggc ttg aat gtc gca ctt atc 509
 Ala Leu Ala Gly Glu Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile
 110 115 120

30

ggc cct gat ctt cct ttt aca aat aac tat ggt gtt tgg gag gat gaa 557
 Gly Pro Asp Leu Pro Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu
 125 130 135

35

ttt ata ggt ctt gga ctt gag ggc tgt att gaa cat gtt tgg cga gat 605
 Phe Ile Gly Leu Gly Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp
 140 145 150 155

40

act gta gta tat ctt gat gac aac gat ccc att ctc ata ggt cgt gcc 653
 Thr Val Val Tyr Leu Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala
 160 165 170

45

tat gga cga gtt agt cgt gat tta ctt cac gag gag ttg ttg act agg 701
 Tyr Gly Arg Val Ser Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg
 175 180 185

tgc atg gag tca ggc gtt tca tat ctg agc tcc aaa gtg gaa cgg att 749
 Cys Met Glu Ser Gly Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile
 190 195 200

71

	act gaa gct cca aat ggc cta agt ctc ata gag tgt gaa ggc aat atc	797
	Thr Glu Ala Pro Asn Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile	
	205 210 215	
5	aca att cca tgc agg ctt gct act gtc gct tct gga gca gct tct gga	845
	Thr Ile Pro Cys Arg Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly	
	220 225 230 235	
10	aaa ctt ttg cag tat gaa ctt ggc ggt ccc cgt gtt tgc gtt caa aca	893
	Lys Leu Leu Gln Tyr Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr	
	240 245 250	
15	gct tat ggt ata gag gtt gag gtt gaa agc ata ccc tat gat cca agc	941
	Ala Tyr Gly Ile Glu Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser	
	255 260 265	
20	cta atg gtt ttc atg gat tat aga gac tac acc aaa cat aaa tct caa	989
	Leu Met Val Phe Met Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln	
	270 275 280	
	tca cta gaa gca caa tat cca aca ttt ttg tat gtc atg cca atg tct	1037
	Ser Leu Glu Ala Gln Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser	
	285 290 295	
25	cca act aaa gta ttc ttt gag gaa act tgt ttg gct tca aaa gag gcc	1085
	Pro Thr Lys Val Phe Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala	
	300 305 310 315	
30	atg cct ttt gag tta ttg aag aca aaa ctc atg tca aga tta aag act	1133
	Met Pro Phe Glu Leu Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr	
	320 325 330	
35	atg ggg atc cga ata acc aaa act tat gaa gag gaa tgg tca tat att	1181
	Met Gly Ile Arg Ile Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile	
	335 340 345	
40	cca gta ggt gga tcc tta cca aat acc gag caa aag aac ctt gca ttt	1229
	Pro Val Gly Gly Ser Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe	
	350 355 360	
	ggt gct gct gct agc atg gtg cat cca gcc aca gga tat tcg gtt gta	1277
	Gly Ala Ala Ala Ser Met Val His Pro Ala Thr Gly Tyr Ser Val Val	
	365 370 375	
45	aga tca ctg tca gaa gct cct aat tat gca gca gta att gca aag att	1325

72

Arg Ser Leu Ser Glu Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile
 380 385 390 395

5 tta ggg aaa gga aat tca aaa cag atg ctt gat cat gga aga tac aca 1373
 Leu Gly Lys Gly Asn Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr
 400 405 410

10 acc aac atc tca aag caa gct tgg gaa aca ctt tgg ccc ctt gaa agg 1421
 Thr Asn Ile Ser Lys Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg
 415 420 425

15 aaa aga cag aga gca ttc ttt ctc ttt gga tta gca ctg att gtc cag 1469
 Lys Arg Gln Arg Ala Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln
 430 435 440

atg gat att gag ggg acc cgc aca ttc ttc cgg act ttc ttc cgc ttg 1517
 Met Asp Ile Glu Gly Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu
 445 450 455

20 ccc aca tgg atg tgg tgg ggg ttt ctt gga tct tcg tta tca tca act 1565
 Pro Thr Trp Met Trp Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr
 460 465 470 475

25 gac ttg ata ata ttt gcg ttt tac atg ttt atc ata gca ccg cat agc 1613
 Asp Leu Ile Ile Phe Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser
 480 485 490

30 ctg aga atg ggt ctg gtt aga cat ttg ctt tct gac ccg aca gga gga 1661
 Leu Arg Met Gly Leu Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly
 495 500 505

35 aca atg tta aaa gcg tat ctc acg ata taa ataactctag tcgcgatcag 1711
 Thr Met Leu Lys Ala Tyr Leu Thr Ile
 510 515

tttagattat aggcacatct tgcataata tatgtataaa ccttatgtgt gctgtatcct 1771

tacatcaaca cagtcattaa ttgtatttct tggggtaatg ctgatgaagt attttctgg 1830

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<210> 39

<211> 516

<212> PRT

<213> Tagetes erecta

5

<400> 39

Met Ser Met Arg Ala Gly His Met Thr Ala Thr Met Ala Ala Phe Thr
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Cys Pro Arg Phe Met Thr Ser Ile Arg Tyr Thr Lys Gln Ile Lys Cys
 15 20 25 30

Asn Ala Ala Lys Ser Gln Leu Val Val Lys Gln Glu Ile Glu Glu Glu
 35 40 45

Glu Asp Tyr Val Lys Ala Gly Gly Ser Glu Leu Leu Phe Val Gln Met
 50 55 60

Gln Gln Asn Lys Ser Met Asp Ala Gln Ser Ser Leu Ser Gln Lys Leu
 65 70 75 80

Pro Arg Val Pro Ile Gly Gly Gly Gly Asp Ser Asn Cys Ile Leu Asp
 30 85 90 95

Leu Val Val Ile Gly Cys Gly Pro Ala Gly Leu Ala Leu Ala Gly Glu
 100 105 110

35

Ser Ala Lys Leu Gly Leu Asn Val Ala Leu Ile Gly Pro Asp Leu Pro
 115 120 125

40

Phe Thr Asn Asn Tyr Gly Val Trp Glu Asp Glu Phe Ile Gly Leu Gly
 130 135 140

45 Leu Glu Gly Cys Ile Glu His Val Trp Arg Asp Thr Val Val Tyr Leu

145		150		155		160
5	Asp Asp Asn Asp Pro Ile Leu Ile Gly Arg Ala Tyr Gly Arg Val Ser	165		170		175
10	Arg Asp Leu Leu His Glu Glu Leu Leu Thr Arg Cys Met Glu Ser Gly	180		185		190
15	Val Ser Tyr Leu Ser Ser Lys Val Glu Arg Ile Thr Glu Ala Pro Asn	195		200		205
20	Gly Leu Ser Leu Ile Glu Cys Glu Gly Asn Ile Thr Ile Pro Cys Arg	210		215		220
25	Leu Ala Thr Val Ala Ser Gly Ala Ala Ser Gly Lys Leu Leu Gln Tyr	225		230		235
30	Glu Leu Gly Gly Pro Arg Val Cys Val Gln Thr Ala Tyr Gly Ile Glu	245		250		255
35	Val Glu Val Glu Ser Ile Pro Tyr Asp Pro Ser Leu Met Val Phe Met	260		265		270
40	Asp Tyr Arg Asp Tyr Thr Lys His Lys Ser Gln Ser Leu Glu Ala Gln	275		280		285
45	Tyr Pro Thr Phe Leu Tyr Val Met Pro Met Ser Pro Thr Lys Val Phe	290		295		300
	Phe Glu Glu Thr Cys Leu Ala Ser Lys Glu Ala Met Pro Phe Glu Leu	305		310		315
	Leu Lys Thr Lys Leu Met Ser Arg Leu Lys Thr Met Gly Ile Arg Ile	325		330		335

Thr Lys Thr Tyr Glu Glu Glu Trp Ser Tyr Ile Pro Val Gly Gly Ser
 340 345 350
 5

Leu Pro Asn Thr Glu Gln Lys Asn Leu Ala Phe Gly Ala Ala Ala Ser
 355 360 365

10 Met, Val His Pro Ala Thr Gly Tyr Ser Val Val Arg Ser Leu Ser Glu
 370 375 380

15 Ala Pro Asn Tyr Ala Ala Val Ile Ala Lys Ile Leu Gly Lys Gly Asn
 385 390 395 400

20 Ser Lys Gln Met Leu Asp His Gly Arg Tyr Thr Thr Asn Ile Ser Lys
 405 410 415

25 Gln Ala Trp Glu Thr Leu Trp Pro Leu Glu Arg Lys Arg Gln Arg Ala
 420 425 430

Phe Phe Leu Phe Gly Leu Ala Leu Ile Val Gln Met Asp Ile Glu Gly
 435 440 445

30 Thr Arg Thr Phe Phe Arg Thr Phe Phe Arg Leu Pro Thr Trp Met Trp
 450 455 460

35 Trp Gly Phe Leu Gly Ser Ser Leu Ser Ser Thr Asp Leu Ile Ile Phe
 465 470 475 480

40 Ala Phe Tyr Met Phe Ile Ile Ala Pro His Ser Leu Arg Met Gly Leu
 485 490 495

45 Val Arg His Leu Leu Ser Asp Pro Thr Gly Gly Thr Met Leu Lys Ala
 500 505 510

Tyr Leu Thr Ile
515

5

<210> 40

<211> 445

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<212> DNA

<213> *Tagetes erecta*

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<220>

<221> Sense Fragment

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<223>

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<400> 40

aagcttgac gaggcaaagc aaaggttggt tgttggtggt gttgagagac actccaatcc 60

aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

30

gaaaaagaat cactactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

35

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

gaaagccggt ggatcggagc tgctttttgt tcaaatacaa cagaataagt ccatggatgc 360

acagtctagc ctatcccaaa agtcccaag ggtaccaata ggaggaggag gagacagtaa 420

40

ctgtatactg gatttggttg tcgac 445

<210> 41

45

<211> 446

<212> DNA

5 <213> Tagetes erecta

<220>

10

<221> Antisense Fragment

<222> (1) .. (446)

15

<223>

<400> 41

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gaattcgac gaggcaaagc aaaggttggt tgttggtggt gttgagagac actccaatcc 60

aaacagatac aaggcgtgac tggatatttc tctctcggtc ctaacaacag caacgaagaa 120

gaaaaagaat cattactaac aatcaatgag tatgagagct ggacacatga cggcaacaat 180

25

ggcggctttt acatgcccta ggtttatgac tagcatcaga tacacgaagc aaattaagtg 240

caacgctgct aaaagccagc tagtcgttaa acaagagatt gaggaggaag aagattatgt 300

30

gaaagccggt ggatcggagc tgctttttgt tcaaagcaa cagaataagt ccatggatgc 360

acagtctagc ctatcccaaa agtcccaag ggtaccaata ggaggaggag gagacagtaa 420

ctgtatactg gatttggttg gaccc 446

35

<210> 42

<211> 393

40

<212> DNA

<213> Tagetes erecta

<220>

5 <221> Sense Fragment

<222> (1)..(393)

<223>

10

<400> 42

15

aagcttttga ttagcactga ttgtccagat ggatattgag gggacccgca cattcttccg 60

gactttcttc cgcttgccca catggatgtg gtggggggtt cttggatctt cgttatcatc 120

aactgacttg ataatatattg cgttttacat gtttatcata gcaccgcata gcctgagaat 180

20

gggtctgggt agacatttgc tttctgaccc gacaggagga acaatgttaa aagcgtatct 240

cacgatataa ataactctag tcgcgatcag ttagattat aggcacatct tgcatatata 300

25

tatgtataaa ccttatgtgt gctgtatcct tacatcaaca cagtcattaa ttgtatttct 360

tggggtaatg ctgatgaagt attttctgtc gac 393

<210> 43

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<211> 397

<212> DNA

35 <213> Tagetes erecta

<220>

40

<221> Antisense Fragment

<222> (1)..(397)

45 <223>

<400> 43
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 tccggacttt ctccgcttg cccacatgga tgtggtgggg gtttcttgga tcttcgttat 120
 catcaactga cttgataata ttgctgtttt acatgtttat catagcaccg catagcctga 180
 10 gaatgggtct ggtagacat ttgctttctg acccgacagg aggaacaatg ttaaaagcgt 240
 atctcagat ataaataact ctagtgcga tcagtttaga ttataggcac atcttgcata 300
 15 tatatatgta taaaccttat gtgtgctgta tccttacatc aacatagtca ttaattgtat 360
 ttcttggggg aatgctgatg aagtattttc tggatcc 397

20 <210> 44

<211> 1537

25 <212> DNA

<213> -

30 <220>

<221> promoter

<222> (1)..(1537)

35 <223>

40 <400> 44
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 tgtacattta ttcaataata ttatatgttt attacaaatt ctcactttct tattcatacc 120
 45 tattcactca agcctttacc atcttccttt tctatttcaa tactatttct acttcatttt 180

	tcacgttttt aacatctttc tttatttctt gtccacttcg tttagggatg cctaattgtcc	240
	caaatttcat ctctcgtagt aacacaaaac caatgtaatg ctacttctct ctacattttt	300
5	aatacaaata aagtgaaaca aaatatctat aaataaaca atatatatat tttgttagac	360
	gctgtctcaa cccatcaatt aaaaaatttt gttatatttc tactttacct actaaatttg	420
10	tttctcatat ttacctttta acccccacaa aaaaaaatta taaaaaagaa agaaaaaagc	480
	taaaccttat ttaaatagct aactataaga tcttaaaatt atcctcatca gtgtatagtt	540
	taattggtta ttaacttata acattatata tctatgacat atactctctc ctagctattt	600
15	ctcacatttt ttaacttaag aaaatagtca taacatagtc taaaattcaa acatccacat	660
	gctctaattt gattaacaaa aagttagaaa tattttattta aataaaaaag actaataaat	720
20	atataaaatg aatgttcata cgcagaccca tttagagatg agtatgcttt cacatgctga	780
	gattattttc aaaactaagg ttgtagcaat attaaatcaa taaaattatt ataaataaca	840
	aaattaacct gctcgtgttt gctgtatatg ggaggctaca aaataaatta aactaaagat	900
25	gattatgttt tagacatttt ttctatctgt attagtttat acatattaat tcaggagctg	960
	cacaacccaa ttctattttc gttccttggt ggctgggttt ctcaacaggt tcaatagtca	1020
30	atattaggtt ttattggact tttaatagta tcaaacaaat ctatgtgtga acttaaaaat	1080
	tgtattaaat atttagggta acctggtgcc gtttttagaa taatgtttct tcttaataca	1140
	cgaaagcgta ttgtgtattc attcatttgg cgctcacat gcttcgggtg gctcgtttta	1200
35	gtctctgcct tctttgtata ttgtactccc cctcttccta tgccacgtgt tctgagctta	1260
	acaagccaag ttgctgcca ttgccaaaca agtcatttta acttcacaag gtccgatttg	1320
40	acctcaaaa caacgacaag ttccgaaca gtcgcgaaga tcaagggat aatcgtcttt	1380
	ttgaattcta tttctcttta tttaatagtc cctctcgtgt gatagttttt aaaagatttt	1440
45	taaaacgtag ctgctgttta agtaaatccc agtccttcag tttgtgcttt tgtgtgtttt	1500

gtttctctga ttacggaat ttggaaataa taagctt

1537

<210> 45

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<211> 734

<212> DNA

10 <213> synthetic sequence

<220>

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<221> variation

<222> (1)..(734)

20 <223>

<400> 45

25 ctaacaatca atgagtagag agctggacac atgacggcaa caatggcggc ttttacatgc 60

cctaggttta tgactagcat cagatacacg aagcaaatta agtgcaacgc tgctaaaagc 120

cagctagtcg ttaaacaaga gattgaggag gaagaagatt atgtgaaagc cggtaggatcg 180

30

gagctgcttt ttgttcaaat gcaacagaat aagtccatgg atgcacagtc tagcctatcc 240

caaaagggtca ctccagactt aattgcttat aaataaataa atatgttttt taggaataat 300

35 gatattttaga tagattagct atcacctgtg ctgtggtgtg cagctcccaa gggctttacc 360

gatagtaaaa tcgttagtta tgattaatac ttgggaggtg ggggattata ggctttgttg 420

tgagaatggt gagaaagagg ttgacaaat cgggtgttga atgagggtta atggagtta 480

40

attaaaataa agagaagaga aagattaaga gggtagatgg gatattaaag acggscaata 540

tagtgatgcc acgtagaaaa aggtaagtga aaacatacaa cgtggcttta aaagatggct 600

45 tggctgctaa tcaactcaac tcaactcata tcctatccat tcaaattcaa ttcaattcta 660

ttgaatgcaa agcaaagcaa aggttgtttg ttgttgttgt tgagagacac tccaatccaa 720
 acagatacaa ggcg 734
 5
 <210> 46
 <211> 280
 10 <212> DNA
 <213> synthetic sequence
 15
 <220>
 <221> variation
 20 <222> (1)..(280)
 <223>
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 <400> 46
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 30 attaaagacg gccaatrtag tgatgccacg taagaaaaag gtaagtgaac acatacaacg 120
 tggctttaa agatggcttg gctgctaata aactcaactc aactcatatc ctatccattc 180
 aaattcaatt caattctatt gaatgcaaag caaagcaaag caaaggttgt ttgttgttgt 240
 35 tgttgagaga cactccaata caaacagata caaggcgtga 280
 <210> 47
 40 <211> 358
 <212> DNA

<213> Tagetes erecta

5 <220>

<221> Sense Promoter

<222> (1) .. (358)

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<223>

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<400> 47

aagcttaccg atagtaaaat cgtaggttat gattaatact tgggaggtgg gggattatag 60

gctttgttgt gagaatgttg agaaagaggt ttgacaaatc ggtgtttgaa tgagggttaa 120

20

tggagtttaa ttaaaataaa gagaagagaa agattaagag ggtgatgggg atattaaaga 180

cggccaatat agtgatgcca cgtagaaaaa ggtaagtga aacatacaac gtggctttaa 240

aagatggctt ggctgctaact caactcaact caactcatat cctatccatt caaattcaat 300

25

tcaattctat tgaatgcaaa gcaaagcaaa gcaaaggttg tttgttggtg ttgtcgac 358

<210> 48

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<211> 361

<212> DNA

35

<213> Tagetes erecta

<220>

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<221> Antisense Promoter

<222> (1) .. (361)

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<223>

<400> 48
 5 ctcgagctta cccatagtaa aatcgtagt tatgattaat acttgggagg tgggggatta 60
 taggctttgt tgtgagaatg ttgagaaaga ggtttgacaa atcgggtgtt gaatgaggtt 120
 aaatggaggtt taattaaaat aaagagaaga gaaagattaa gagggatgatg gggatattaa 180
 10 agacggccaa tatagtgatg ccacgtagaa aaaggtaagt gaaaacatac aacgtggctt 240
 taaaagatgg cttggctgct aatcaactca actcaactca taccctatcc attcaaattc 300
 15 aattcaattc tattgaatgc aaagcaaagc aaagcaaagg ttgtttgttg ttgttgatc 360
 c 361

20 <210> 49

<211> 28

<212> DNA

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<213> synthetic sequence

30 <220>

<221> Primer

<222> (1)..(28)

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<223>

40 <400> 49

gagctcactc actgatttcc attgcttg

28

<210> 50

45

<211> 37

<212> DNA

5 <213> synthetic sequence

<220>

10

<221> Primer

<222> (1)..(37)

15

<223>

<400> 50

20 cgccggttaag tcgatgtccg ttgatttaaa cagtgtc

37

<210> 51

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<211> 34

<212> DNA

<213> synthetic sequence

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<220>

35

<221> Primer

<222> (1)..(34)

<223>

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<400> 51

45 atcaacggac atcgacttaa cggcgtttgt aaac

34

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30
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45

<210> 52
<211> 25
<212> DNA
<213> synthetic sequence
<220>
<221> Primer
<222> (1)..(25)
<223>
<400> 52
taagcttttt gttgaagaga tttgg
<210> 53
<211> 23
<212> DNA
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<222> (1)..(23)
<223>

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<400> 53

gaaaatacctt catcagcatt acc

23

5 <210> 54

<211> 28

<212> DNA

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<213> synthetic sequence

15 <220>

<221> Primer

<222> (1)..(28)

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<223>

25 <400> 54

gtcgactacg taagtttctg cttctacc

28

<210> 55

30

<211> 26

<212> DNA

35 <213> synthetic sequence

<220>

40

<221> Primer

<222> (1)..(26)

45 <223>

5 <400> 55
ggatccggtg atacctgcac atcaac

26

10 <210> 56

<211> 28

<212> DNA

15 <213> synthetic sequence

<220>

20 <221> Primer

<222> (1) .. (28)

25 <223>

30 <400> 56
aagcttgcac gaggcaaagc aaaggttg

28

<210> 57

35 <211> 29

<212> DNA

<213> synthetic sequence

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<220>

45 <221> Primer

<222> (1)..(29)

<223>

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<400> 57

gtcgacaacc aaatccagta tacagttac

29

10

<210> 58

<211> 30

15

<212> DNA

<213> synthetic sequence

20

<220>

<221> Primer

25

<222> (1)..(30)

<223>

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<400> 58

aggatccaac caaatccagt atacagttac

30

35

<210> 59

<211> 28

<212> DNA

40

<213> synthetic sequence

<220>

<221> Primer

5 <222> (1)..(28)

<223>

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<400> 59

gaattcgcac gaggcaaagc aaaggttg

28

15

<210> 60

<211> 25

<212> DNA

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<213> synthetic sequence

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<220>

<221> Primer

<222> (1)..(25)

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<223>

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<400> 60

aagctttgga ttagcactga ttgtc

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<210> 61

<211> 29

<212> DNA

<213> synthetic sequence

5 <220>

<221> Primer

<222> (1)..(29)

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<223>

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<400> 61

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29

20

<210> 62

<211> 29

<212> DNA

25

<213> synthetic sequence

30

<220>

<221> Primer

<222> (1)..(29)

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<223>

40

<400> 62

ggatccagaa aatacttcat cagcattac

29

<210> 63

<211> 27

<212> DNA

5 <213> synthetic sequence

<220>

10

<221> Primer

<222> (1)..(27)

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<223>

<400> 63

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<210> 64

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<211> 23

<212> DNA

<213> synthetic sequence

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<220>

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<221> Primer

<222> (1)..(23)

<223>

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<400> 64

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23

<210> 65

<211> 24

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<212> DNA

<213> synthetic sequence

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<220>

<221> Primer

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<222> (1)..(24)

<223>

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<400> 65

ctaacaatca atgagtatga gagc

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<210> 66

<211> 26

30

<212> DNA

<213> synthetic sequence

35

<220>

<221> Primer

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<222> (1)..(26)

<223>

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<400> 66
agagcaaggc cagcaggacc acaacc

26

5 <210> 67

<211> 26

<212> DNA

10

<213> synthetic sequence

15 <220>

<221> Primer

<222> (1)..(26)

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<223>

25 <400> 67

ccttgggagc ttttgggata ggctag

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<210> 68

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<211> 26

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35 <213> synthetic sequence

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<221> Primer

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5 tcacgccttg tatctgtttg gattgg

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<210> 69

10 <211> 15

<212> DNA

<213> , synthetic sequence

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<220>

20 <221> Primer

<222> (1)..(15)

<223>

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<400> 69

30 gtcgagtatg gagtt

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<210> 70

<211> 28

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<212> DNA

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<220>

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<222> (1)..(28)

<223>

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<400> 70

aagcttaccg atagtaaaat cgttagtt

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<210> 71

<211> 31

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<213> synthetic sequence

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<222> (1)..(31)

<223>

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<400> 71

ctcgagctta ccgatagtaa aatcgtagt t

31

35

<210> 72

<211> 28

<212> DNA

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<213> synthetic sequence

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<400> 72

gtcgacaaca acaacaaaca acctttgc

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<210> 73

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<211> 28

<212> DNA

10 <213> synthetic sequence

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<221> Primer

<222> (1)..(28)

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25 ggatccaaca acaacaaaca acctttgc

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<210> 74

30 <211> 28

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40 <221> Primer

<222> (1)..(28)

<223>

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5 <400> 74
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10 <210> 75

<211> 28

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<223>

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<210> 76

<211> 22

35 <212> DNA

<213> synthetic sequence

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<222> (1)..(22)

<223>

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<400> 76

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22

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<211> 23

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<222> (1)..(23)

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aagcttatta tttccaaatt ccg

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<223>

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50

15

<210> 79

<211> 1062

<212> DNA

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<213> Haematococcus pluvialis

25

<220>

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<222> (32)..(1021)

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<223>

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<400> 79

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52

Met Gln Leu Ala Ala Thr Val

1

5

40

atg ttg gag cag ctt acc gga agc gct gag gca ctc aag gag aag gag

100

Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys Glu Lys Glu

10

15

20

aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg gcg acc cag

148

45

Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp Ala Thr Gln

	25	30	35	
	tac tcg ctt ccg tca gag gag tca gac gcg gcc cgc ccg gga ctg aag			196
5	Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro Gly Leu Lys			
	40	45	50	55
	aat gcc tac aag cca cca cct tcc gac aca aag ggc atc aca atg gcg			244
	Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile Thr Met Ala			
10		60	65	70
	cta gct gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac gcc att ttt			292
	Leu Ala Val Ile Gly Ser Trp Ala Ala Val Phe Leu His Ala Ile Phe			
	75	80	85	
15	caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg ctg ccc gtg			340
	Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp Leu Pro Val			
	90	95	100	
	tca gat gcc aca gct cag ctg gtt agc ggc agc agc agc ctg ctg cac			388
20	Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Ser Ser Ser Leu Leu His			
	105	110	115	
	atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca ggc ctt ttt			436
	Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe			
25	120	125	130	135
	atc acc acg cat gat gct atg cat ggc acc atc gcc atg aga aac agg			484
	Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met Arg Asn Arg			
	140	145	150	
30	cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg tac gcc tgg			532
	Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu Tyr Ala Trp			
	155	160	165	
35	ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac cac aac cac			580
	Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His His Asn His			
	170	175	180	
	act ggc gag gtg ggc aag gac cct gac ttc cac agg gga aac cct ggc			628
40	Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly Asn Pro Gly			
	185	190	195	
	att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg tcg atg tgg			676
	Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Met Trp			
45	200	205	210	215

cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag ctg ctg ggt 724
 Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln Leu Leu Gly
 220 225 230

5

gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg ccc atc ctg 772
 Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu
 235 240 245

10

tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc cac aag cct 820
 Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro His Lys Pro
 250 255 260

15

gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg aac tgg tgg 868
 Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met Asn Trp Trp
 265 270 275

20

aag tgc cgc act agc cag gcg tcc gac ctg gtc agc ttt ctg acc tgc 916
 Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe Leu Thr Cys
 280 285 290 295

25

tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc ttt gcc ccc 964
 Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro
 300 305 310

30

tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga ggt ctg gtt 1012
 Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 315 320 325

35

cct gcc tag ctggacacac tgcagtgggc cctgctgccca gctgggcatg c 1062
 Pro Ala

40

<210> 80
 <211> 329
 <212> PRT
 <213> Haematococcus pluvialis

45

<400> 80

1 Met Glu Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
 1 5 10 15

5 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
 20 25 30

10 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

15 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

20 Thr Lys Gly Ile Thr Met Ala Leu Ala Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
 85 90 95

25 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
 100 105 110

30 Gly Ser Ser Ser Leu Leu His Ile Val Val Val Phe Phe Val Leu Glu
 115 120 125

35 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
 130 135 140

40 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
 145 150 155 160

Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
 165 170 175

45

104

His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
 180 185 190

5 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
 195 200 205

10 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
 210 215 220

15 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
 225 230 235 240

Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
 245 250 255

20 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
 260 265 270

25 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
 275 280 285

30 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
 290 295 300

35 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
 305 310 315 320

Leu Ser Gly Arg Gly Leu Val Pro Ala
 325

40 <210> 81

<211> 789

<212> DNA

<213> Nostoc punctiforme

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<220>

<221> CDS

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<222> (1)..(789)

<223>

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ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa 48

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln

20

1

5

10

15

tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg' att gtc ata gta 96

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val

20

25

30

25

att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat 144

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn

35

40

45

30

tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa 192

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln

50

55

60

atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat 240

35

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His

65

70

75

80

ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca 288

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser

40

85

90

95

cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag 336

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys

100

105

110

45

106

aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat 384
 Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

5 ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc 432
 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

10 atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta 480
 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

15 ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc 528
 Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

20 tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat 576
 Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat 624
 Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

25 ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc 672
 Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

30 gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat 720
 Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

35 gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac 768
 Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

40 aat tca gta acc aat tcg taa 789
 Asn Ser Val Thr Asn Ser
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<210> 82

<211> 262

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<212> PRT

<213> Nostoc punctiforme

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<400> 82

10 Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
1 5 10 15

15 Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
35 40 45

20 Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
50 55 60

25 Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
65 70 75 80

30 Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
85 90 95

35 Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
115 120 125

40 Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
130 135 140

45 Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu

145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
5 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
10 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
15 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
20 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
25 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
30 245 250 255

Asn Ser Val Thr Asn Ser
35 260

<210> 83

<211> 762

<212> DNA

<213> Nostoc punctiforme

<220>

<221> CDS

45

<223>

<400> . 83

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15

20

25

30

35

40

45

atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att 480
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile

110

	145	150	155	160	
	tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act				528
	Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr				
5		165	170	175	
	tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat				576
	Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr				
	180		185	190	
10	ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag				624
	Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln				
	195		200	205	
15	cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc				672
	Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile				
	210		215	220	
	acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat				720
20	Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His				
	225		230	235	240
	att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag				762
	Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys				
25		245	250		
	<210> 84				
30	<211> 253				
	<212> PRT				
	<213> Nostoc punctiforme				
35					
	<400> 84				
40	Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro				
	1	5	10	15	
	Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val				
45	20		25	30	

5

10

15

20

25

30

35

40

45

Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln
195 200 205

Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile
 210 215 220

5

Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

10 Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys
 245 250

<210> .85

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<211> 804

<212> DNA

20 <213> Synechococcus WH8102

<220>

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<221> CDS

<222> (1)..(804)

30 <223>

<400> 85

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 Met Lys Thr Thr Arg Ser Ile Ser Trp Pro Ser Thr Cys Trp His His
 1 5 10 15

cag ccg agt tgc tca agc tgg gtg gca aat gag ttc agc cct cag gcc 96
 40 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30

ctc aaa ggg ttg gct ctg gct ggt ctg att gga tca gcc tgg ctg ctc 144
 45 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45

113

	tcc ctg ggc ctg agc tac acc ctg cca ctt gat cag acg cct ggg ctg	192
	Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu	
	50 55 60	
5	ttg att ggc agc ttg att ctg ctc aga gca ttt ctg cac acc ggg ctg	240
	Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu	
	65 70 75 80	
10	ttc atc gtt gcc cac gat tcc atg cac gcc agt ctg gtt ccg ggt cat	288
	Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His	
	85 90 95	
15	ccc gga ttg aac cgc tgg atc ggc aaa gtg tat ttg ttg gtg tat gca	336
	Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala	
	100 105 110	
20	ggc ttg tct tat gag cgt tgt tcc cgc aac cac aga cgt cat cac ctg	384
	Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu	
	115 120 125	
25	gca ccg gag acg ttc cag gat cct gac tac caa cgt tgc acc aat aac	432
	Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn	
	130 135 140	
30	aac atc cta gat tgg tat gtt cac ttc atg ggc aac tat ctg ggc atg	480
	Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met	
	145 150 155 160	
35	cgg caa ctg tta aat cta agc tgt ctt tgg ctg gcg cta atc att ctc	528
	Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu	
	165 170 175	
40	aac ggt tct gat ctc cct gct cag atc atg cat ctg ctg ttg ttc agc	576
	Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser	
	180 185 190	
45	gtt ctg ccg ttg atc atc agt tcc tgt caa ttg ttt cta gtg gga acc	624
	Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr	
	195 200 205	
50	tgg tta ccc cac cga cgt ggg gcc acg aca cga ccg ggc gtg aca acg	672
	Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr	
	210 215 220	

114

cgc agc ctg gct ttg cat cca gcc ctc tct ttc gca gct tgt tac aac 720
 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240

5 ttt ggc tat cat cgt gaa cat cat gaa tcg cct tcc aca ccc tgg ttt 768
 Phe Gly Tyr His Arg Glu His His Glu Ser Pro Ser Thr Pro Trp Phe
 245 250 255

10 cag ctg cca caa ctt cga aat gaa tca ttc act tga 804
 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr
 260 265

15 <210> 86
 <211> 267
 <212> PRT

20 <213> Synechococcus WH8102

25 <400> 86
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 1 5 10 15

30 Gln Pro Ser Cys Ser Ser Trp Val Ala Asn Glu Phe Ser Pro Gln Ala
 20 25 30

35 Leu Lys Gly Leu Ala Leu Ala Gly Leu Ile Gly Ser Ala Trp Leu Leu
 35 40 45

40 Ser Leu Gly Leu Ser Tyr Thr Leu Pro Leu Asp Gln Thr Pro Gly Leu
 50 55 60

45 Leu Ile Gly Ser Leu Ile Leu Leu Arg Ala Phe Leu His Thr Gly Leu
 65 70 75 80

115

Phe Ile Val Ala His Asp Ser Met His Ala Ser Leu Val Pro Gly His
 85 90 95

5 Pro Gly Leu Asn Arg Trp Ile Gly Lys Val Tyr Leu Leu Val Tyr Ala
 100 105 110

10 Gly Leu Ser Tyr Glu Arg Cys Ser Arg Asn His Arg Arg His His Leu
 115 120 125

15 Ala Pro Glu Thr Phe Gln Asp Pro Asp Tyr Gln Arg Cys Thr Asn Asn
 130 135 140

20 Asn Ile Leu Asp Trp Tyr Val His Phe Met Gly Asn Tyr Leu Gly Met
 145 150 155 160

Arg Gln Leu Leu Asn Leu Ser Cys Leu Trp Leu Ala Leu Ile Ile Leu
 165 170 175

25 Asn Gly Ser Asp Leu Pro Ala Gln Ile Met His Leu Leu Leu Phe Ser
 180 185 190

30 Val Leu Pro Leu Ile Ile Ser Ser Cys Gln Leu Phe Leu Val Gly Thr
 195 200 205

35 Trp Leu Pro His Arg Arg Gly Ala Thr Thr Arg Pro Gly Val Thr Thr
 210 215 220

40 Arg Ser Leu Ala Leu His Pro Ala Leu Ser Phe Ala Ala Cys Tyr Asn
 225 230 235 240

45 Gln Leu Pro Gln Leu Arg Asn Glu Ser Phe Thr

260

265

5 <210> 87

<211> 33

<212> DNA

10 <213> synthetic sequence

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<400> 87

25 gcattgctcta gaccttataa agatattttg tga

33

<210> 88

30 <211> 33

<212> DNA

<213> synthetic sequence

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40 <221> primer_bind

<222> (1)..(33)

<223>

45

<400> 88
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<210> 89
 <211> 805
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 <213> Nostoc sp. Strain PCC7120
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 <222> (1)..(805)
 <223>
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 ttatcttatt tttatgggca attagtttaa tcttattact ctcaatagat acatccataa 180
 ttcataagag cttattaggt atagccatgc tttggcagac cttcttatat acagggtttat 240
 35 ttattactgc tcatgatgcc atgcacggcg tagtttatcc caaaaatccc agaataaata 300
 attttatagg taagctcact ctaatcttgt atggactact cccttataaa gatttattga 360
 40 aaaaacattg gttacaccac ggacatcctg gtactgattt agaccctgat tattacaatg 420
 gtcacccca aaacttcttt ctttggtatc tacattttat gaagtcttat tggcgatgga 480
 cgcaaatttt cggattagtg atgatttttc atggacttaa aaatctggtg catataccag 540
 45

118

aaaataattt aattatattt tggatgatac cttctatttt aagttcagta caactatttt 600
at ttgtgttac at ttgtgcct cataaaaagc tagaagggtgg ttataactaac cccattgtg 660
5 cgcgcagtat cccattacct cttttttggt cttttgttac ttgttatcac ttcggctacc 720
acaaggaaca tcacgaatac cctcaacttc cttggtggaa attacctgaa gtcacaaaaa 780
tatctttata aggtctagag catgc 805

10

<210> 90

<211> 35

15

<212> DNA

<213> synthetic sequence

20

<220>

<221> primer_bind

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<223>

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<400> 90

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<210> 91

<211> 44

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<212> DNA

<213> synthetic sequence

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<223>
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<400> 91
aagcttgagc tcggttgatc agaagaagaa gaagaagatg aact 44
15 <210> 92
<211> 653
<212> DNA
20 <213> Arabidopsis thaliana
25 <220>
<221> promoter
<222> (1)..(653)
30 <223>
35 <400> 92
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taatacttta cccgtgtaaa tcaaaaacaa aaaggctttt gagctttttg tagttgaatt 120
40 tctctggctg atcttttctg tacagattca tatatctgca gagacgatat cattgattat 180
ttgagcttct tttgaactat ttcgtgtaat ttgggatgag agctctatgt atgtgtgtaa 240
actttgaaga caacaagaaa ggtaacaagt gagggagggg tgactccatg tcaaaataga 300
45

120

tgtcataaga ggcccatcaa taagtgcttg agcccattag ctagcccagt aactaccaga 360
ttgtgagatg gatgtgtgaa cagttttttt ttgatgtag gactgaaatg tgaacaacag 420
5 gcgcatgaaa ggctaaatta ggacaatgat aagcagaaat aacttatcct ctctaact 480
tggcctcaca ttgcccttca cacaatccac acacatccaa tcacaacctc atcatatc 540
tcccgctaata ctttttttct ttgatctttt tttttttgct tattattttt ttgactttga 600
10 tctcccatca gttcatcttc ttcttcttct tctgatcaac cgagctcaag ctt 653

<210> 93

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<211> 28

<212> DNA

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<213> synthetic sequence

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<223>

<400> 93

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gagctcactc actgatttcc attgcttg

28

<210> 94

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<211> 30

<212> DNA

<213> synthetic sequence

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<220>

5 <221> primer_bind

<222> (1)..(30)

<223>

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<400> 94

aagcttgagc tctttgttga agagatttgg

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15

<210> 95

<211> 37

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<212> DNA

<213> synthetic sequence

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<220>

<221> primer_bind

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<222> (1)..(37)

<223>

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<400> 95

cgccgttaag tcgatgtccg ttgatttaaa cagtgtc

37

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<210> 96

<211> 34

<212> DNA

<213> synthetic sequence

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<222> (1)..(34)

<223>

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<400> 96

atcaacggac atcgacttaa cggcgtttgt aaac

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<210> 97

<211> 831

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<212> DNA

<213> *Haematococcus pluvialis*

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<222> (1)..(831)

<223>

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<400> 97

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Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Val Leu Lys His Ala

48

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10

15

45

123

	tat aaa cct cca gca tct gac gcc aag ggc atc act atg gcg ctg acc	96
	Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr	
	20 25 30	
5	atc att ggc acc tgg acc gca gtg ttt tta cac gca ata ttc caa atc	144
	Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile	
	35 40 45	
10	agg cta ccg aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa	192
	Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu	
	50 55 60	
15	gcc aca gcc cag ctg ttg ggc gga agc agc agc cta ttg cac atc gcc	240
	Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala	
	65 70 75 80	
20	gca gtc ttc att gta ctt gag ttt ctg tac act ggt cta ttc atc acc	288
	Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr	
	85 90 95	
25	acg cat gat gca atg cat ggc acc ata gct ttg agg aac agg cag ctc	336
	Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu	
	100 105 110	
30	aat gat ctc ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac	384
	Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp	
	115 120 125	
35	tac agc atg cac tgg gag cac cac aac cat act ggc gaa gtg ggg aaa	432
	Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys	
	130 135 140	
40	gac cct gac ttc cac aaa gga aat cct ggc ctt gtc ccc tgg ttc gcc	480
	Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala	
	145 150 155 160	
45	agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg gca	528
	Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala	
	165 170 175	
50	tgg tgg gca gtg gtg atg caa acg ttg ggg gcc ccc atg gcg aat ctc	576
	Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu	
	180 185 190	
55	cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc ttc	624

124

Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
 195 200 205

5 tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca gca 672
 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
 210 215 220

10 ggc tct cag gtc atg tct tgg ttc agg gcc aag aca agt gag gca tct 720
 Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
 225 230 235 240

15 gat gtg atg agc ttc ctg aca tgc tac cac ttt gac ctg ttt gcc ccc 768
 Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
 245 250 255

15 tgg tgg cag ctg ccc cac tgc cgc cgc ctg tct ggg cgt ggc ctg gtg 816
 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

20 cct gcc ttg gca tga 831
 Pro Ala Leu Ala
 275

25 <210> 98
 <211> 276
 <212> PRT

30 <213> Haematococcus pluvialis

35 <400> 98
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40 Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
 20 25 30

45 Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile

35

40

45

5 Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
50 55 60

10 Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
65 70 75 80

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
85 90 95

15 Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg Asn Arg Gln Leu
100 105 110

20 Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
115 120 125

25 Tyr Ser Met His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys
130 135 140

30 Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe Ala
145 150 155 160

Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu Ala
165 170 175

35 Trp Trp Ala Val Val Met Gln Thr Leu Gly Ala Pro Met Ala Asn Leu
180 185 190

40 Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe
195 200 205

45 Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala Ala
210 215 220

Gly Ser Gln Val Met Ser Trp Phe Arg Ala Lys Thr Ser Glu Ala Ser
 225 230 235 240
 5

Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu Phe Ala Pro
 245 250 255

10 Trp Trp Gln Leu Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val
 260 265 270

15 Pro Ala Leu Ala
 275

20 <210> 99
 <211> 729
 <212> DNA

25 <213> Paracoccus sp. MBIC1143

30 <220>
 <221> CDS
 <222> (1)..(729)

35 <223>

<400> 99
 40 atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc acc agc ctg 48
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

45 atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

127

	20	25	30	
5	gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala	144		
	35	40	45	
10	aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala	192		
	50	55	60	
15	cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn	240		
	65	70	75	80
20	gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	288		
	85	90	95	
25	cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	336		
	100	105	110	
30	gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	384		
	115	120	125	
35	cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	432		
	130	135	140	
40	gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	480		
	145	150	155	160
45	gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	528		
	165	170	175	
50	gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	576		
	180	185	190	
55	gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	624		
	195	200	205	

ctg acc tgc ttt cac ttt ggc ggt tat tat cac gaa cac cac ctg cac 672
 Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

5

ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac 720
 Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

10

acc gca tga 729
 Thr Ala

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<210> 100
 <211> 242
 <212> PRT

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<213> Paracoccus sp. MBIC1143

25

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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
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Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

35

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

40

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

45

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala, Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
85 90 95

5

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
100 105 110

10

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
115 120 125

15

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
130 135 140

20

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

25

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
180 185 190

30

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
195 200 205

35

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
210 215 220

40

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
225 230 235 240

Thr Ala

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<210> 101

<211> 735

5 <212> DNA

<213> Brevundimonas aurantiaca

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<220>

<221> CDS

15 <222> (1)..(735)

<223>

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<400> 101

atg acc gcc gcc gtc gcc gag cca cgc acc gtc ccg cgc cag acc tgg 48
 Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
 1 5 10 15

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atc ggt ctg acc ctg gcg gga atg atc gtg gcg gga tgg gcg gtt ctg 96
 Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu
 20 25 30

30

cat gtc tac ggc gtc tat ttt cac cga tgg ggg ccg ttg acc ctg gtg 144
 His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val
 35 40 45

35

atc gcc ccg gcg atc gtg gcg gtc cag acc tgg ttg tcg gtc ggc ctt 192
 Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu
 50 55 60

40

ttc atc gtc gcc cat gac gcc atg tac ggc tcc ctg gcg ccg gga cgg 240
 Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

ccg cgg ctg aac gcc gca gtc ggc cgg ctg acc ctg ggg ctc tat gcg 288
 Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

45

131

ggc ttc cgc ttc gat cgg ctg aag acg gcg cac cac gcc cac cac gcc 336
 Gly Phe, Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

5 gcg ccc ggc acg gcc gac gac ccg gat ttt cac gcc ccg gcg ccc cgc 384
 Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg
 115 120 125

10 gcc ttc ctt ccc tgg ttc ctg aac ttc ttt cgc acc tat ttc ggc tgg 432
 Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

15 cgc gag atg gcg gtc ctg acc gcc ctg gtc ctg atc gcc ctc ttc ggc 480
 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly
 145 150 155 160

20 ctg ggg gcg cgg ccg gcc aat ctc ctg acc ttc tgg gcc gcg ccg gcc 528
 Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
 165 170 175

ctg ctt tca gcg ctt cag ctc ttc acc ttc ggc acc tgg ctg ccg cac 576
 Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
 180 185 190

25 cgc cac acc gac cag ccg ttc gcc gac gcg cac cac gcc cgc agc agc 624
 Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
 195 200 205

30 ggc tac ggc ccc gtg ctt tcc ctg ctc acc tgt ttc cac ttc ggc cgc 672
 Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
 210 215 220

35 cac cac gaa cac cat ctg agc ccc tgg cgg ccc tgg tgg cgt ctg tgg 720
 His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
 225 230 235 240

cgc ggc gag tct tga 735
 Arg Gly Glu Ser

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<210> 102

<211> 244

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<212> PRT

<213> Brevundimonas aurantiaca

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<400> 102

Met Thr Ala Ala Val Ala Glu Pro Arg Thr Val Pro Arg Gln Thr Trp
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Ile Gly Leu Thr Leu Ala Gly Met Ile Val Ala Gly Trp Ala Val Leu
 20 25 30

15

His Val Tyr Gly Val Tyr Phe His Arg Trp Gly Pro Leu Thr Leu Val
 35 40 45

20

Ile Ala Pro Ala Ile Val Ala Val Gln Thr Trp Leu Ser Val Gly Leu
 50 55 60

Phe Ile Val Ala His Asp Ala Met Tyr Gly Ser Leu Ala Pro Gly Arg
 65 70 75 80

Pro Arg Leu Asn Ala Ala Val Gly Arg Leu Thr Leu Gly Leu Tyr Ala
 85 90 95

30

Gly Phe Arg Phe Asp Arg Leu Lys Thr Ala His His Ala His His Ala
 100 105 110

35

Ala Pro Gly Thr Ala Asp Asp Pro Asp Phe His Ala Pro Ala Pro Arg
 115 120 125

40

Ala Phe Leu Pro Trp Phe Leu Asn Phe Phe Arg Thr Tyr Phe Gly Trp
 130 135 140

45 Arg Glu Met Ala Val Leu Thr Ala Leu Val Leu Ile Ala Leu Phe Gly

145 150 155 160

Leu Gly Ala Arg Pro Ala Asn Leu Leu Thr Phe Trp Ala Ala Pro Ala
5 165 170 175

Leu Leu Ser Ala Leu Gln Leu Phe Thr Phe Gly Thr Trp Leu Pro His
10 180 185 190

Arg His Thr Asp Gln Pro Phe Ala Asp Ala His His Ala Arg Ser Ser
15 195 200 205

Gly Tyr Gly Pro Val Leu Ser Leu Leu Thr Cys Phe His Phe Gly Arg
210 215 220

His His Glu His His Leu Ser Pro Trp Arg Pro Trp Trp Arg Leu Trp
20 225 230 235 240

Arg Gly Glu Ser
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<210> 103

30 <211> 690

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<212> DNA

<213> Nodularia spumigena NSOR10
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<220>

40 <221> CDS

<222> (1)..(690)

<223>
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<400> 103

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Met Ala Ile Ala Ile Ile Ser Ile Trp Ala Ile Ser Leu Gly Leu Leu
1 5 10 15

10 ctt tat att gat ata tcc caa ttc aag ttt tgg atg ttg tta ccg ctc 96
Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
20 25 30

15 ata ttt tgg caa aca ttt tta tat acg gga tta ttt att aca gct cat 144
Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
35 40 45

gat gcc atg cat ggg gta gtt ttt ccc aaa aat ccc aaa atc aac cat 192
Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
50 55 60

20 ttc att ggc tca ttg tgc ctg ttt ctt tat ggt ctt tta cct tat caa 240
Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
65 70 75 80

25 aaa ctt tta aaa aag cat tgg cta cat cac cat aat cca gcc agt gaa 288
Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
85 90 95

30 aca gat cca gat ttt cac aac ggg aag cag aaa aac ttt ttt gct tgg 336
Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
100 105 110

35 tat tta tat ttt atg aag cgt tac tgg agt tgg tta caa att atc aca 384
Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
115 120 125

tta atg att att tat aac tta cta aaa tat ata tgg cat ttt cca gag 432
Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
130 135 140

40 gat aat atg act tat ttt tgg gta gtt ccc tca att tta agt tct tta 480
Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
145 150 155 160

45 caa tta ttt tat ttt gga act ttt cta ccc cac agt gag cct gta gaa 528
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu

135

165

170

175

5 ggt tat aaa gag cct cat cgt tcc caa act att agc cgt ccc att tgg 576
 Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 180 185 190

10 tgg tca ttt ata act tgt tac cat ttt ggt tat cat tac gaa cat cat 624
 Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 195 200 205

gaa tac ccc cat gtt cct tgg tgg caa tta cca gaa att tat aaa atg 672
 Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220

15 tct aaa tca aat ttg tga 690
 Ser Lys Ser Asn Leu
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20 <210> 104
 <211> 229
 <212> PRT

25 <213> Nodularia spumigena NSOR10

30 <400> 104
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35 Leu Tyr Ile Asp Ile Ser Gln Phe Lys Phe Trp Met Leu Leu Pro Leu
 20 25 30

40 Ile Phe Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 35 40 45

45 Asp Ala Met His Gly Val Val Phe Pro Lys Asn Pro Lys Ile Asn His
 50 55 60

Phe Ile Gly Ser Leu Cys Leu Phe Leu Tyr Gly Leu Leu Pro Tyr Gln
 65 70 75 80
 5

Lys Leu Leu Lys Lys His Trp Leu His His His Asn Pro Ala Ser Glu
 85 90 95
 10

Thr Asp Pro Asp Phe His Asn Gly Lys Gln Lys Asn Phe Phe Ala Trp
 100 105 110
 15

Tyr Leu Tyr Phe Met Lys Arg Tyr Trp Ser Trp Leu Gln Ile Ile Thr
 115 120 125
 20

Leu Met Ile Ile Tyr Asn Leu Leu Lys Tyr Ile Trp His Phe Pro Glu
 130 135 140
 25

Asp Asn Met Thr Tyr Phe Trp Val Val Pro Ser Ile Leu Ser Ser Leu
 145 150 155 160
 30

Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Ser Glu Pro Val Glu
 165 170 175
 35

Gly Tyr Lys Glu Pro His Arg Ser Gln Thr Ile Ser Arg Pro Ile Trp
 180 185 190
 40

Trp Ser Phe Ile Thr Cys Tyr His Phe Gly Tyr His Tyr Glu His His
 195 200 205
 45

Glu Tyr Pro His Val Pro Trp Trp Gln Leu Pro Glu Ile Tyr Lys Met
 210 215 220
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Ser Lys Ser Asn Leu
 225

<210> 105

<211> 1536

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<212> DNA

<213> Deinococcus radiodurans R1

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<220>

<221> CDS

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<222> (1)..(1536)

<223>

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<400> 105

atg ccg gat tac gac ctg atc gtc atg ggc gcg ggc cac aac gcg ctg 48

Met Pro Asp Tyr Asp Leu Ile Val Met Gly Ala Gly His Asn Ala Leu

25

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5

10

15

gtg act gct gcc tac gcc gcc cgg gcg ggc ctg aaa gtc ggc gtg ttc 96

Val Thr Ala Ala Tyr Ala Ala Arg Ala Gly Leu Lys Val Gly Val Phe

20

25

30

30

gag cgg cgg gac ctc gtc ggc ggg gcg gtc agc acc gag gag gtc gtg 144

Glu Arg Arg His Leu Val Gly Gly Ala Val Ser Thr Glu Glu Val Val

35

40

45

35

ccc ggt tac cgc ttc gac tac ggc ggc agc gcc cac atc ctg att cgg 192

Pro Gly Tyr Arg Phe Asp Tyr Gly Gly Ser Ala His Ile Leu Ile Arg

50

55

60

atg acg ccc atc gtg cgc gaa ctc gaa ctc acg cgg cac ggg ctg cat 240

Met Thr Pro Ile Val Arg Glu Leu Glu Leu Thr Arg His Gly Leu His

40

65

70

75

80

tac ctc gaa gtg gac cct atg ttt cac gct tcc gac ggt gaa acg ccc 288

Tyr Leu Glu Val Asp Pro Met Phe His Ala Ser Asp Gly Glu Thr Pro

45

85

90

95

	tgg ttc, att cac cgc gac gcc ggg cgg acc atc cgc gaa ctg gac gaa	336
	Trp Phe Ile His Arg Asp Ala Gly Arg Thr Ile Arg Glu Leu Asp Glu	
	100 105 110	
5	aag ttt ccc ggg cag ggc gac gcc tac ggg cgc ttt ctc gac gat tgg	384
	Lys Phe Pro Gly Gln Gly Asp Ala Tyr Gly Arg Phe Leu Asp Asp Trp	
	115 120 125	
10	aca ccc ttc gcg cgc gcc gtg gcc gac ctg ttc aac tcg gcg ccg ggg	432
	Thr Pro Phe Ala Arg Ala Val Ala Asp Leu Phe Asn Ser Ala Pro Gly	
	130 135 140	
	ccg ctc gac ctg ggc aaa atg gtg atg cgc agc ggc cag ggc aag gac	480
15	Pro Leu Asp Leu Gly Lys Met Val Met Arg Ser Gly Gln Gly Lys Asp	
	145 150 155 160	
	tgg aac gag cag ctc ccg cgc atc ctg cgg ccc tac ggc gac gtg gcg	528
20	Trp Asn Glu Gln Leu Pro Arg Ile Leu Arg Pro Tyr Gly Asp Val Ala	
	165 170 175	
	cgc gag tac ttc agc gag gag cgc gtg cgg gct ccc ctg acc tgg atg	576
	Arg Glu Tyr Phe Ser Glu Glu Arg Val Arg Ala Pro Leu Thr Trp Met	
	180 185 190	
25	gcg gcc cag agc ggc ccc cca ccc tcg gac ccg ctg agc gcg ccc ttt	624
	Ala Ala Gln Ser Gly Pro Pro Ser Asp Pro Leu Ser Ala Pro Phe	
	195 200 205	
30	ttg ctg tgg cac ccg ctc tac cac gaa ggc ggc gtg gcg cgg ccc aaa	672
	Leu Leu Trp His Pro Leu Tyr His Glu Gly Gly Val Ala Arg Pro Lys	
	210 215 220	
	ggc ggc agc ggc ggc ctg acc aaa gcc ctg cgc cgg gcc acc gag gcc	720
35	Gly Gly Ser Gly Gly Leu Thr Lys Ala Leu Arg Arg Ala Thr Glu Ala	
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	gaa ggc ggc gag gtc ttc acc gac gcg ccg gtc aag gaa att ctg gtc	768
40	Glu Gly Gly Glu Val Phe Thr Asp Ala Pro Val Lys Glu Ile Leu Val	
	245 250 255	
	aag gac ggc aag gcg cag ggc atc cgg ctg gaa agc ggc gag acg tac	816
	Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr	
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139

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	Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn	
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	Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val	
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	Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val	
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	Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu	
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	Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu	
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	Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser	
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	Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu	
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	Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr	
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	Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr	
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	Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro	
	420 425 430	
	cag tgg ctg gaa acc aac ctc ggc ctg cac cgg ggc aac gtg atg cac	1344
	Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His	
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140

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	gcg	gcg	cgg	gtc	atc	gtg	aag	gac	ctg	acg	cgg	agg	cgc	tgg	aaa	tga	1536
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	Pro	Gly	Tyr	Arg	Phe	Asp	Tyr	Gly	Gly	Ser	Ala	His	Ile	Leu	Ile	Arg	
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10	Trp	Phe	Ile	His	Arg	Asp	Ala	Gly	Arg	Thr	Ile	Arg	Glu	Leu	Asp	Glu	
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			115					120					125				
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40	Ala	Ala	Gln	Ser	Gly	Pro	Pro	Pro	Ser	Asp	Pro	Leu	Ser	Ala	Pro	Phe	
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Lys Asp Gly Lys Ala Gln Gly Ile Arg Leu Glu Ser Gly Glu Thr Tyr
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Thr Ala Arg Ala Val Val Ser Gly Val His Ile Leu Thr Thr Ala Asn
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Ala Leu Pro Ala Glu Tyr Val Pro Ser Ala Ala Arg Asn Val Arg Val
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Gly Asn Gly Phe Gly Met Ile Leu Arg Leu Ala Leu Ser Glu Lys Val
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Lys Tyr Arg His His Thr Glu Pro Asp Ser Arg Ile Gly Leu Gly Leu
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Leu Ile Lys Asn Glu Arg Gln Ile Met Gln Gly Tyr Gly Glu Tyr Leu
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Ala Gly Gln Pro Thr Thr Asp Pro Pro Leu Val Ala Met Ser Phe Ser
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Ala Val Asp Asp Ser Leu Ala Pro Pro Asn Gly Asp Val Leu Trp Leu
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Trp Ala Gln Tyr Tyr Pro Phe Glu Leu Ala Thr Gly Ser Trp Glu Thr
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Arg Thr Ala Glu Ala Arg Glu Asn Ile Leu Arg Ala Phe Glu His Tyr
 405 410 415

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Ala Pro Gly Thr Arg Asp Thr Ile Val Gly Glu Leu Val Gln Thr Pro
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143

Gln Trp Leu Glu Thr Asn Leu Gly Leu His Arg Gly Asn Val Met His
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Leu Glu Met Ser Phe Asp Gln Met Phe Ser Phe Arg Pro Trp Leu Lys
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Ala Ser Gln Tyr Arg Trp Pro Gly Val Gln Gly Leu Tyr Leu Thr Gly
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	Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser	
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	Lys Leu Phe Cys Ser Phe Leu Asp Leu Ala Pro Thr Ser Lys Pro Glu	
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	Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala	
	65 70 75 80	
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	Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu	
	85 90 95	
25	gct gaa caa gtt tct aaa tat ggt att aag gta tgt tgt gtt gac cct	336
	Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro	
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	Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu	
	115 120 125	
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	Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met	
	130 135 140	
40	act tgt gtg cat ata aat gat aac aaa act aag tat ttg gga aga cca	480
	Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro	
	145 150 155 160	
45	tat ggt aga gtt agt aga aag aag ctg aag ttg aaa ttg ttg aat agt	528
	Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser	
	165 170 175	
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	Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val	
	180 185 190	

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	gaa cat gaa gaa ttt gag tct tca att gtt tgt gat gat ggt aag aag	624
	Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys	
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	Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe	
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	Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly	
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	260 265 270	
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	275 280 285	
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	Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val	
	290 295 300	
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	Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His	
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	Leu Gly Ile Lys Val Lys Ser Val Ile Glu Glu Glu Lys Cys Val Ile	
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	Pro Met Gly Gly Pro Leu Pro Arg Ile Pro Gln Asn Val Met Ala Ile	
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146

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25	ttc ctt tct tca aga ttg tct gtc aaa gaa ctt ggt tta ctc agc ttg Phe Leu Ser Ser Arg Leu Ser Val Lys Glu Leu Gly Leu Leu Ser Leu	1392
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	465 470 475 480	
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	485 490 495	
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Thr Thr Lys Lys Lys Ser Arg Lys Cys Leu Leu Arg Asn Lys Ser Ser
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Ser Leu Asp Val Asn Ile Ser Trp Val Asp Pro Asn Ser Asn Arg Ala
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Gln Phe Asp Val Ile Ile Ile Gly Ala Gly Pro Ala Gly Leu Arg Leu
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Ala Glu Gln Val Ser Lys Tyr Gly Ile Lys Val Cys Cys Val Asp Pro
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Ser Pro Leu Ser Met Trp Pro Asn Asn Tyr Gly Val Trp Val Asp Glu
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Phe Glu Asn Leu Gly Leu Glu Asn Cys Leu Asp His Lys Trp Pro Met
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Thr Cys Val His Ile Asn Asp Asn Lys Thr Lys Tyr Leu Gly Arg Pro
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Tyr Gly Arg Val Ser Arg Lys Lys Leu Lys Leu Lys Leu Leu Asn Ser
 165 170 175

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Cys Val Glu Asn Arg Val Lys Phe Tyr Lys Ala Lys Val Trp Lys Val
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Glu His Glu Glu Phe Glu Ser Ser Ile Val Cys Asp Asp Gly Lys Lys
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Ile Arg Gly Ser Leu Val Val Asp Ala Ser Gly Phe Ala Ser Asp Phe
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Ile Glu Tyr Asp Arg Pro Arg Asn His Gly Tyr Gln Ile Ala His Gly
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Val Leu Val Glu Val Asp Asn His Pro Phe Asp Leu Asp Lys Met Val
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Leu Met Asp Trp Arg Asp Ser His Leu Gly Asn Glu Pro Tyr Leu Arg
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Val Asn Asn Ala Lys Glu Pro Thr Phe Leu Tyr Ala Met Pro Phe Asp
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Arg Asp Leu Val Phe Leu Glu Glu Thr Ser Leu Val Ser Arg Pro Val
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Leu Ser Tyr Met Glu Val Lys Arg Arg Met Val Ala Arg Leu Arg His
 305 310 315 320

149

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 Cys Phe Val Leu Glu Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu
 60 65 70 75
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151

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5	Leu	Ala	Glu	Lys	Leu	Ala	Arg	Lys	Lys	Ser	Glu	Arg	Phe	Thr	Tyr	Leu	
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	gtg	gct	gct	ata	atg	tct	agt	ttt	ggg	att	act	tct	atg	gct	gtt	atg	388
10	Val	Ala	Ala	Ile	Met	Ser	Ser	Phe	Gly	Ile	Thr	Ser	Met	Ala	Val	Met	
				110					115				120				
	gct	gtt	tat	tac	aga	ttt	tcg	tgg	caa	atg	gag	gga	gga	gaa	gtt	cct	436
	Ala	Val	Tyr	Tyr	Arg	Phe	Ser	Trp	Gln	Met	Glu	Gly	Gly	Glu	Val	Pro	
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15	gta	acc	gaa	atg	ttg	ggt	aca	ttt	gct	ctc	tct	gtt	ggt	gct	gct	gta	484
	Val	Thr	Glu	Met	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Val	Gly	Ala	Ala	Val	
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20	Gly	Met	Glu	Phe	Trp	Ala	Arg	Trp	Ala	His	Lys	Ala	Leu	Trp	His	Ala	
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	Phe	Glu	Leu	Asn	Asp	Val	Phe	Ala	Ile	Thr	Asn	Ala	Val	Pro	Ala	Ile	
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	gcc	ctc	ctc	aac	tat	ggt	ttc	ttc	cat	aaa	ggc	ctc	att	gcc	gga	cta	676
	Ala	Leu	Leu	Asn	Tyr	Gly	Phe	Phe	His	Lys	Gly	Leu	Ile	Ala	Gly	Leu	
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	Cys	Phe	Gly	Ala	Gly	Leu	Gly	Ile	Thr	Val	Phe	Gly	Met	Ala	Tyr	Met	
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40	Phe	Val	His	Asp	Gly	Leu	Val	His	Lys	Arg	Phe	Pro	Val	Gly	Pro	Val	
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	Ile Arg Arg Thr Arg Leu Ser Lys Gly Ser			
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	tagagaaaaa tgtagctctc ttgatgaaat gaatttgat ttatgtaggc tcttcttatt			1086
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40				
	Ser His Val Ser Pro Ile Ser Pro Phe Ser Leu Asn Leu Gly Pro Ile			
	35	40	45	
45				

153

Leu Arg Ser Arg Arg Lys Pro Ser Phe Thr Val Cys Phe Val Leu Glu
 50 55 60

5 Asp Glu Lys Leu Lys Pro Gln Phe Asp Asp Glu Ala Glu Asp Phe Glu
 65 70 75 80

10 Lys Lys Ile Glu Glu Gln Ile Leu Ala Thr Arg Leu Ala Glu Lys Leu
 85 90 95

15 Ala Arg Lys Lys Ser Glu Arg Phe Thr Tyr Leu Val Ala Ala Ile Met
 100 105 110

Ser Ser Phe Gly Ile Thr Ser Met Ala Val Met Ala Val Tyr Tyr Arg
 115 120 125

20 Phe Ser Trp Gln Met Glu Gly Gly Glu Val Pro Val Thr Glu Met Leu
 130 135 140

25 Gly Thr Phe Ala Leu Ser Val Gly Ala Ala Val Gly Met Glu Phe Trp
 145 150 155 160

30 Ala Arg Trp Ala His Lys Ala Leu Trp His Ala Ser Leu Trp His Met
 165 170 175

35 His Glu Ser His His Lys Pro Arg Glu Gly Pro Phe Glu Leu Asn Asp
 180 185 190

Val Phe Ala Ile Thr Asn Ala Val Pro Ala Ile Ala Leu Leu Asn Tyr
 195 200 205

40 Gly Phe Phe His Lys Gly Leu Ile Ala Gly Leu Cys Phe Gly Ala Gly
 210 215 220

45 Leu Gly Ile Thr Val Phe Gly Met Ala Tyr Met Phe Val His Asp Gly

225

230

235

240

5

Leu Val His Lys Arg Phe Pro Val Gly Pro Val Ala Asn Val Pro Tyr
 245 250 255

10

Leu Arg Lys Val Ala Ala Ala His Ser Leu His His Ser Glu Lys Phe
 260 265 270

15

Asn Gly Val Pro Tyr Gly Leu Phe Phe Gly Pro Lys Glu Leu Glu Glu
 275 280 285

Val Gly Gly Thr Glu Glu Leu Glu Lys Glu Val Ile Arg Arg Thr Arg
 290 295 300

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Leu Ser Lys Gly Ser
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<220>

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<223>

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48

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	1				5					10					15		
	aac tcc aac gga tct ttc cgt tct tat cag cct cgc act tcc gat gac																96
5	Asn	Ser	Asn	Gly	Ser	Phe	Arg	Ser	Tyr	Gln	Pro	Arg	Thr	Ser	Asp	Asp	
			20						25					30			
	gat cat cgt cgc cgg gct aca aca att gct cct cca ccg aaa gca tcc																144
10	Asp	His	Arg	Arg	Arg	Ala	Thr	Thr	Ile	Ala	Pro	Pro	Pro	Lys	Ala	Ser	
			35					40					45				
	gac gcg ctt cct ctt ccg tta tat ctc aca aac gcc gtt ttc ttc acg																192
	Asp	Ala	Leu	Pro	Leu	Pro	Leu	Tyr	Leu	Thr	Asn	Ala	Val	Phe	Phe	Thr	
15			50				55					60					
	ctc ttc ttc tcc gtc gcg tat tac ctc ctc cac cgg tgg cgt gac aag																240
	Leu	Phe	Phe	Ser	Val	Ala	Tyr	Tyr	Leu	Leu	His	Arg	Trp	Arg	Asp	Lys	
			65			70				75					80		
20	atc cgt tac aat acg cct ctt cac gtc gtc act atc aca gaa ctc ggc																288
	Ile	Arg	Tyr	Asn	Thr	Pro	Leu	His	Val	Val	Thr	Ile	Thr	Glu	Leu	Gly	
				85					90					95			
	gcc att att gct ctc atc gct tcg ttt atc tat ctc cta ggg ttt ttt																336
25	Ala	Ile	Ile	Ala	Leu	Ile	Ala	Ser	Phe	Ile	Tyr	Leu	Leu	Gly	Phe	Phe	
				100					105					110			
	ggc att gac ttt gtt cag tca ttt atc tca cgt gcc tct ggt gat gct																384
30	Gly	Ile	Asp	Phe	Val	Gln	Ser	Phe	Ile	Ser	Arg	Ala	Ser	Gly	Asp	Ala	
			115				120					125					
	tgg gat ctc gcc gat acg atc gat gat gat gac cac cgc ctt gtc acg																432
	Trp	Asp	Leu	Ala	Asp	Thr	Ile	Asp	Asp	Asp	Asp	His	Arg	Leu	Val	Thr	
35			130				135					140					
	tgc tct cca ccg act ccg atc gtt tcc gtt gct aaa tta cct aat ccg																480
	Cys	Ser	Pro	Pro	Thr	Pro	Ile	Val	Ser	Val	Ala	Lys	Leu	Pro	Asn	Pro	
			145			150				155			160				
40	gaa cct att gtt acc gaa tcg ctt cct gag gaa gac gag gag att gtg																528
	Glu	Pro	Ile	Val	Thr	Glu	Ser	Leu	Pro	Glu	Glu	Asp	Glu	Glu	Ile	Val	
				165					170				175				
	aaa tcg gtt atc gac gga gtt att cca tcg tac tcg ctt gaa tct cgt																576
45	Lys	Ser	Val	Ile	Asp	Gly	Val	Ile	Pro	Ser	Tyr	Ser	Leu	Glu	Ser	Arg	

	180	185	190	
	ctc ggt gat tgc aaa aga gcg gcg tcg att cgt cgt gag gcg ttg cag			624
	Leu Gly Asp Cys Lys Arg Ala Ala Ser Ile Arg Arg Glu Ala Leu Gln			
5	195	200	205	
	aga gtc acc ggg aga tcg att gaa ggg tta ccg ttg gat gga ttt gat			672
	Arg Val Thr Gly Arg Ser Ile Glu Gly Leu Pro Leu Asp Gly Phe Asp			
	210	215	220	
10				
	tat gaa tcg att ttg ggg caa tgc tgt gag atg cct gtt gga tac att			720
	Tyr Glu Ser Ile Leu Gly Gln Cys Cys Glu Met Pro Val Gly Tyr Ile			
	225	230	235	240
15	cag att cct gtt ggg att gct ggt cca ttg ttg ctt gat ggt tat gag			768
	Gln Ile Pro Val Gly Ile Ala Gly Pro Leu Leu Leu Asp Gly Tyr Glu			
	245	250	255	
	tac tct gtt cct atg gct aca acc gaa ggt tgt ttg gtt gct agc act			816
20	Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr			
	260	265	270	
	aac aga ggc tgc aag gct atg ttt atc tct ggt ggc gcc acc agt acc			864
	Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr			
25	275	280	285	
	ggt ctt aag gac ggt atg acc cga gca cct gtt gtt cgg ttc gct tcg			912
	Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser			
	290	295	300	
30				
	gcg aga cga gct tcg gag ctt aag ttt ttc ttg gag aat cca gag aac			960
	Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn			
	305	310	315	320
35	ttt gat act ttg gca gta gtc ttc aac agg tcg agt aga ttt gca aga			1008
	Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg			
	325	330	335	
	ctg caa agt gtt aaa tgc aca atc gcg ggg aag aat gct tat gta agg			1056
40	Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg			
	340	345	350	
	ttc tgt tgt agt act ggt gat gct atg ggg atg aat atg gtt tct aaa			1104
	Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys			
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	ggt gtg cag aat gtt ctt gag tat ctt acc gat gat ttc cct gac atg Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met 370 375 380	1152
5	gat gtg att gga atc tct ggt aac ttc tgt tcg gac aag aaa cct gct Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala 385 390 395 400	1200
10	gct gtg aac tgg att gag gga cgt ggt aaa tca gtt gtt tgc gag gct Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala 405 410 415	1248
15	gta atc aga gga gag atc gtg aac aag gtc ttg aaa acg agc gtg gct Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala 420 425 430	1296
20	gct tta gtc gag ctc aac atg ctc aag aac cta gct ggc tct gct gtt Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val 435 440 445	1344
25	gca ggc tct cta ggt gga ttc aac gct cat gcc agt aac ata gtg tct Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser 450 455 460	1392
30	gct gta ttc ata gct act ggc caa gat cca gct caa aac gtg gag agt Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser 465 470 475 480	1440
35	tct caa tgc atc acc atg atg gaa gct att aat gac ggc aaa gat atc Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile 485 490 495	1488
40	cat atc tca gtc act atg cca tct atc gag gtg ggg aca gtg gga gga His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly 500 505 510	1536
45	gga aca cag ctt gca tct caa tca gcg tgt tta aac ctg ctc gga gtt Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val 515 520 525	1584
	aaa gga gca agc aca gag tcg ccg gga atg aac gca agg agg cta gcg Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala 530 535 540	1632

158

acg atc gta gcc gga gca gtt tta gct gga gag tta tct tta atg tca 1680
 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
 545 550 555 560

5 gca att gca gct gga cag ctt gtg aga agt cac atg aaa tac aat aga 1728
 Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

10 tcc agc cga gac atc tct gga gca acg aca acg aca aca aca aca 1776
 Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr
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tga 1779

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 20 25 30

35 Asp His Arg Arg Arg Ala Thr Thr Ile Ala Pro Pro Pro Lys Ala Ser
 35 40 45

40 Asp Ala Leu Pro Leu Pro Leu Tyr Leu Thr Asn Ala Val Phe Phe Thr
 50 55 60

45 Leu Phe Phe Ser Val Ala Tyr Tyr Leu Leu His Arg Trp Arg Asp Lys
 65 70 75 80

5

10

15

20

25

30

35

40

45

160

Tyr Ser Val Pro Met Ala Thr Thr Glu Gly Cys Leu Val Ala Ser Thr
 260 265 270

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Asn Arg Gly Cys Lys Ala Met Phe Ile Ser Gly Gly Ala Thr Ser Thr
 275 280 285

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Val Leu Lys Asp Gly Met Thr Arg Ala Pro Val Val Arg Phe Ala Ser
 290 295 300

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Ala Arg Arg Ala Ser Glu Leu Lys Phe Phe Leu Glu Asn Pro Glu Asn
 305 310 315 320

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Phe Asp Thr Leu Ala Val Val Phe Asn Arg Ser Ser Arg Phe Ala Arg
 325 330 335

Leu Gln Ser Val Lys Cys Thr Ile Ala Gly Lys Asn Ala Tyr Val Arg
 340 345 350

25

Phe Cys Cys Ser Thr Gly Asp Ala Met Gly Met Asn Met Val Ser Lys
 355 360 365

30

Gly Val Gln Asn Val Leu Glu Tyr Leu Thr Asp Asp Phe Pro Asp Met
 370 375 380

35

Asp Val Ile Gly Ile Ser Gly Asn Phe Cys Ser Asp Lys Lys Pro Ala
 385 390 395 400

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Ala Val Asn Trp Ile Glu Gly Arg Gly Lys Ser Val Val Cys Glu Ala
 405 410 415

Val Ile Arg Gly Glu Ile Val Asn Lys Val Leu Lys Thr Ser Val Ala
 420 425 430

45

161

Ala Leu Val Glu Leu Asn Met Leu Lys Asn Leu Ala Gly Ser Ala Val
 435 440 445

5 Ala Gly Ser Leu Gly Gly Phe Asn Ala His Ala Ser Asn Ile Val Ser
 450 455 460

10 Ala Val Phe Ile Ala Thr Gly Gln Asp Pro Ala Gln Asn Val Glu Ser
 465 470 475 480

Ser Gln Cys Ile Thr Met Met Glu Ala Ile Asn Asp Gly Lys Asp Ile
 485 490 495

15 His Ile Ser Val Thr Met Pro Ser Ile Glu Val Gly Thr Val Gly Gly
 500 505 510

20 Gly Thr Gln Leu Ala Ser Gln Ser Ala Cys Leu Asn Leu Leu Gly Val
 515 520 525

25 Lys Gly Ala Ser Thr Glu Ser Pro Gly Met Asn Ala Arg Arg Leu Ala
 530 535 540

30 Thr Ile Val Ala Gly Ala Val Leu Ala Gly Glu Leu Ser Leu Met Ser
 545 550 555 560

Ala Ile Ala Ala Gly Gln Leu Val Arg Ser His Met Lys Tyr Asn Arg
 565 570 575

35 Ser Ser Arg Asp Ile Ser Gly Ala Thr Thr Thr Thr Thr Thr Thr Thr
 580 585 590

40 <210> 113
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1 5 10 15

ttc gtg cgg gag aat cat ctc tct gga tcc gga tct ctc cgc cgc cgg 96
 Phe Val Arg Glu Asn His Leu Ser Gly Ser Gly Ser Leu Arg Arg Arg

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20 25 30

aaa gct tta tca gtc cgg tgc tcg tct ggc gat gag aac gct cct tcg 144
 Lys Ala Leu Ser Val Arg Cys Ser Ser Gly Asp Glu Asn Ala Pro Ser

30

35 40 45

cca tcg gtg gtg atg gac tcc gat ttc gac gcc aag gtg ttc cgt aag 192
 Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys

35

50 55 60

aac ttg acg aga agc gat aat tac aat cgt aaa ggg ttc ggt cat aag 240
 Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys

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65 70 75 80

gag gag aca ctc aag ctc atg aat cga gag tac acc agt gat ata ttg 288
 Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu

45

85 90 95

gag aca ctg aaa aca aat ggg tat act tat tct tgg gga gat gtt act 336
 Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr

100

105

110

163

	gtg aaa ctc gct aaa gca tat ggt ttt tgc tgg ggt gtt gag cgt gct Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala 115 120 125	384
5	ggt cag att gca tat gaa gca cga aag cag ttt cca gag gag agg ctt Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu 130 135 140	432
10	tgg att act aac gaa atc att cat aac ccg acc gtc aat aag agg ttg Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu 145 150 155 160	480
15	gaa gat atg gat gtt aaa att att ccg gtt gag gat tca aag aaa cag Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln 165 170 175	528
20	ttt gat gta gta gag aaa gat gat gtg gtt atc ctt cct gcg ttt gga Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly 180 185 190	576
	gct ggt gtt gac gag atg tat gtt ctt aat gat aaa aag gtg caa att Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile 195 200 205	624
25	ggt gac acg act tgt cct tgg gtg aca aag gtc tgg aac acg gtt gag Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu 210 215 220	672
30	aag cac aag aag ggg gaa tac aca tca gta atc cat ggt aaa tat aat Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn 225 " 230 235 240	720
35	cat gaa gag acg att gca act gcg tct ttt gca gga aag tac atc att His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile 245 250 255	768
40	gta aag aac atg aaa gag gca aat tac gtt tgt gat tac att ctc ggt Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly 260 265 270	816
	ggc caa tac gat gga tct agc tcc aca aaa gag gag ttc atg gag aaa Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys 275 280 285	864
45	ttc aaa tac gca att tcg aag ggt ttc gat ccc gac aat gac ctt gtc	912

164

Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
290 295 300

aaa gtt ggt att gca aac caa aca acg atg cta aag gga gaaaca gag
5 Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
305 310 315 320

gag ata gga aga tta ctc gag aca aca atg atg cgc aag tat gga gtg 1008
Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val
10 325 330 335

gaa aat gta agc gga cat ttc atc agc ttc aac aca ata tgc gac gct 1056
Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala
340 345 350

act caa gag cga caa gac gca atc tat gag cta gtg gaa gag aag att 1104
Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile
355 360 365

20 gac ctc atg cta gtg gtt ggc gga tgg aat tca agt aac acc tct cac . 1152
Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
370 375 380

25 ctt cag gaa atc tca gag gca cgg gga atc cca tct tac tgg atc gat 1200
 Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
 385 390 395 400

30 agt gag aaa cgg ata gga cct ggg aat aaa ata gcc tat aag ctc cac 1248
Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
405 410 415

tat gga gaa ctg gtc gag aag gaa aac ttt ctc cca aag gga cca ata 1296
Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
420 425 430

aca atc ggt gtg aca tca ggt gca tca acc ccg gat aag gtc gtg gaa 1344
Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
435 440 445

40 gat gct ttg gtg aag gtg ttc gac att aaa cgt gaa gag tta ttg cag 1392
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Leu Ala

1401

465

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<211> 466

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 35 40 45

30 Pro Ser Val Val Met Asp Ser Asp Phe Asp Ala Lys Val Phe Arg Lys
 50 55 60

Asn Leu Thr Arg Ser Asp Asn Tyr Asn Arg Lys Gly Phe Gly His Lys
 65 70 75 80

35

Glu Glu Thr Leu Lys Leu Met Asn Arg Glu Tyr Thr Ser Asp Ile Leu
 85 90 95

40 Glu Thr Leu Lys Thr Asn Gly Tyr Thr Tyr Ser Trp Gly Asp Val Thr
 100 105 110

45 Val Lys Leu Ala Lys Ala Tyr Gly Phe Cys Trp Gly Val Glu Arg Ala
 115 120 125

Val Gln Ile Ala Tyr Glu Ala Arg Lys Gln Phe Pro Glu Glu Arg Leu
 130 135 140
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Trp Ile Thr Asn Glu Ile Ile His Asn Pro Thr Val Asn Lys Arg Leu
 145 150 155 160

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Glu Asp Met Asp Val Lys Ile Ile Pro Val Glu Asp Ser Lys Lys Gln
 165 170 175

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Phe Asp Val Val Glu Lys Asp Asp Val Val Ile Leu Pro Ala Phe Gly
 180 185 190

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Ala Gly Val Asp Glu Met Tyr Val Leu Asn Asp Lys Lys Val Gln Ile
 195 200 205

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Val Asp Thr Thr Cys Pro Trp Val Thr Lys Val Trp Asn Thr Val Glu
 210 215 220

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Lys His Lys Lys Gly Glu Tyr Thr Ser Val Ile His Gly Lys Tyr Asn
 225 230 235 240

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His Glu Glu Thr Ile Ala Thr Ala Ser Phe Ala Gly Lys Tyr Ile Ile
 245 250 255

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Val Lys Asn Met Lys Glu Ala Asn Tyr Val Cys Asp Tyr Ile Leu Gly
 260 265 270

Gly Gln Tyr Asp Gly Ser Ser Ser Thr Lys Glu Glu Phe Met Glu Lys
 275 280 285

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Phe Lys Tyr Ala Ile Ser Lys Gly Phe Asp Pro Asp Asn Asp Leu Val
 290 295 300

Lys Val Gly Ile Ala Asn Gln Thr Thr Met Leu Lys Gly Glu Thr Glu
305 310 315 320

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Glu Ile Gly Arg Leu Leu Glu Thr Thr Met Met Arg Lys Tyr Gly Val
325 330 335

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Glu Asn Val Ser Gly His Phe Ile Ser Phe Asn Thr Ile Cys Asp Ala
340 345 350

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Thr Gln Glu Arg Gln Asp Ala Ile Tyr Glu Leu Val Glu Glu Lys Ile
355 360 365

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Asp Leu Met Leu Val Val Gly Gly Trp Asn Ser Ser Asn Thr Ser His
370 375 380

25
Leu Gln Glu Ile Ser Glu Ala Arg Gly Ile Pro Ser Tyr Trp Ile Asp
385 390 395 400

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Ser Glu Lys Arg Ile Gly Pro Gly Asn Lys Ile Ala Tyr Lys Leu His
405 410 415

35
Tyr Gly Glu Leu Val Glu Lys Glu Asn Phe Leu Pro Lys Gly Pro Ile
420 425 430

40
Thr Ile Gly Val Thr Ser Gly Ala Ser Thr Pro Asp Lys Val Val Glu
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Asp Ala Leu Val Lys Val Phe Asp Ile Lys Arg Glu Glu Leu Leu Gln
450 455 460

Leu Ala
465

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<211> 2160

5 <212> DNA

<213> Lycopersicon esculentum

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15 <222> (1)..(2160)

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<400> 115

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gtg gtt tca gat tct tct aag gca acc cct ttg ttc tct gga tgg att 96

Val Val Ser Asp Ser Ser Lys Ala Thr Pro Leu Phe Ser Gly Trp Ile

20 25 30

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cat gga aca gat ctg cag ttt ttg ttc caa cac aag ctt act cat gag 144

His Gly Thr Asp Leu Gln Phe Leu Phe Gln His Lys Leu Thr His Glu

35 40 45

35

gtc aag aaa agg tca cgt gtg gtt cag gct tcc tta tca gaa tct gga 192

Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly

50 55 60

40

gaa tac tac aca cag aga ccg cca acg cct att ttg gac act gtg aac 240

Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn

65 70 75 80

tat ccc att cat atg aaa aat ctg tct ctg aag gaa ctt aaa caa cta 288

Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu

85 90 95

45

169

	gca gat gaa cta agg tca gat aca att ttc aat gta tca aag act ggg	336
	Ala Asp, Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly	
	100 105 110	
5	ggc cac ctt ggc tca agt ctt ggt gtt gtt gag ctg act gtt gct ctt	384
	Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu	
	115 120 125	
10	cat tat gtc ttc aat gca ccg caa gat agg att ctc tgg gat gtt ggt	432
	His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly	
	130 135 140	
15	cat cag tct tat cct cac aaa atc ttg act ggt aga agg gac aag atg	480
	His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met	
	145 150 155 160	
20	tcg aca tta agg cag aca gat ggt ctt gca gga ttt act aag cga tcg	528
	Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser	
	165 170 175	
	gag agt gaa tat gat tgc ttt ggc acc ggc cac agt tcc acc acc atc	576
	Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile	
	180 185 190	
25	tca gca ggc cta ggg atg gct gtt ggt aga gat cta aaa gga aga aac	624
	Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn	
	195 200 205	
30	aac aat gtt att gcc gta ata ggt gat ggt gcc atg aca gca ggt caa	672
	Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln	
	210 215 220	
35	gct tat gaa gcc atg aat aat gct ggt tac ctg gac tct gac atg att	720
	Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile	
	225 230 235 240	
40	gtt atc tta aac gac aat aga caa gtt tct tta cct act gct act ctg	768
	Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu	
	245 250 255	
	gat ggg cca gtt gct cct gtt gga gct cta agt agt gct ttg agc agg	816
	Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg	
	260 265 270	
45	tta cag tct aat agg cct ctc aga gaa cta aga gaa gtc gca aag gga	864

	Leu	Gln	Ser	Asn	Arg	Pro	Leu	Arg	Glu	Leu	Arg	Glu	Val	Ala	Lys	Gly		
	275						280						285					
5	gtt	act	aag	cag	att	ggt	ggt	cct	atg	cat	gag	ctt	gct	gca	aaa	ggt	912	
	Val	Thr	Lys	Gln	Ile	Gly	Gly	Pro	Met	His	Glu	Leu	Ala	Ala	Lys	Val		
	290					295					300							
10	gat	gaa	tat	gct	cgt	ggc	atg	att	agt	ggg	tct	gga	tca	aca	ttg	ttt	960	
	Asp	Glu	Tyr	Ala	Arg	Gly	Met	Ile	Ser	Gly	Ser	Gly	Ser	Thr	Leu	Phe		
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15	gaa	gaa	ctt	gga	ctt	tac	tat	att	ggg	cct	gtg	gat	ggg	cac	aac	att	1008	
	Glu	Glu	Leu	Gly	Leu	Tyr	Tyr	Ile	Gly	Pro	Val	Asp	Gly	His	Asn	Ile		
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	Asp	Asp	Leu	Ile	Ala	Ile	Leu	Lys	Glu	Val	Arg	Ser	Thr	Lys	Thr	Thr		
	340								345					350				
25	ggg	cca	gta	ctg	atc	cat	gtt	gtc	act	gag	aaa	ggc	aga	ggg	tat	cca	1104	
	Gly	Pro	Val	Leu	Ile	His	Val	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Pro		
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30	tat	gct	gag	aga	gct	gca	gat	aag	tat	cat	gga	gtt	gcc	aag	ttt	gat	1152	
	Tyr	Ala	Glu	Arg	Ala	Ala	Asp	Lys	Tyr	His	Gly	Val	Ala	Lys	Phe	Asp		
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	Thr	Thr	Tyr	Phe	Ala	Glu	Ala	Leu	Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys		
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45	gac	att	gtt	gca	atc	cat	gct	gcc	atg	ggg	ggg	ggg	acc	gga	atg	aac	1296	
	Asp	Ile	Val	Ala	Ile	His	Ala	Ala	Met	Gly	Gly	Gly	Thr	Gly	Met	Asn		
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50	ctt	ttc	cat	cgt	cgc	ttc	cca	aca	agg	tgt	ttt	gat	gtt	gga	ata	gca	1344	
	Leu	Phe	His	Arg	Arg	Phe	Pro	Thr	Arg	Cys	Phe	Asp	Val	Gly	Ile	Ala		
	435							440					445					
55	gaa	caa	cat	gca	gta	acc	ttt	gct	gct	gga	ttg	gct	tgt	gaa	ggc	att	1392	
	Glu	Gln	His	Ala	Val	Thr	Phe	Ala	Ala	Gly	Leu	Ala	Cys	Glu	Gly	Ile		

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	Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp			
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	cag gta gtg cat gac gtt gat ttg caa aag ctg ccc gtg agg ttt gca			
	Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala			
	485	490	495	
10	atg gac aga gca ggt ctt gtt gga gca gat ggt cca aca cat tgt ggt			
	Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly			
	500	505	510	
15	gca ttt gat gtt act tac atg gca tgt ctt cdt aac atg gtt gta atg			
	Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met			
	515	520	525	
	gct cct tct gat gaa gcg gag cta ttt cac atg gta gca act gct gcc			
20	Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala			
	530	535	540	
	gcc att gat gac aga cca agt tgt ttt aga tac cca aga gga aat ggg			
	Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly			
25	545	550	555	560
	atc ggt gta gag ctt ccg gct gga aac aaa gga att cct ctt gag gtt			
	Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val			
	565	570	575	
30	ggt aaa ggt agg ata ttg att gag ggg gag aga gtg gct cta ttg gga			
	Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly			
	580	585	590	
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	Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu			
	595	600	605	
	tcc cgc ggc tta caa gta aca gtt gca gat gca cgt ttc tgc aaa cca			
40	Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro			
	610	615	620	
	ctg gac cat gcc ctc ata agg agc ctt gca aaa tca cat gaa gtg cta			
	Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu			
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Val Lys Lys Arg Ser Arg Val Val Gln Ala Ser Leu Ser Glu Ser Gly
 50 55 60

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Glu Tyr Tyr Thr Gln Arg Pro Pro Thr Pro Ile Leu Asp Thr Val Asn
 65 70 75 80

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Tyr Pro Ile His Met Lys Asn Leu Ser Leu Lys Glu Leu Lys Gln Leu
 85 90 95

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Ala Asp Glu Leu Arg Ser Asp Thr Ile Phe Asn Val Ser Lys Thr Gly
 100 105 110

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Gly His Leu Gly Ser Ser Leu Gly Val Val Glu Leu Thr Val Ala Leu
 115 120 125

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His Tyr Val Phe Asn Ala Pro Gln Asp Arg Ile Leu Trp Asp Val Gly
 130 135 140

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His Gln Ser Tyr Pro His Lys Ile Leu Thr Gly Arg Arg Asp Lys Met
 145 150 155 160

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Ser Thr Leu Arg Gln Thr Asp Gly Leu Ala Gly Phe Thr Lys Arg Ser
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Glu Ser Glu Tyr Asp Cys Phe Gly Thr Gly His Ser Ser Thr Thr Ile
 180 185 190

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Ser Ala Gly Leu Gly Met Ala Val Gly Arg Asp Leu Lys Gly Arg Asn
 195 200 205

Asn Asn Val Ile Ala Val Ile Gly Asp Gly Ala Met Thr Ala Gly Gln
 210 215 220

174

Ala Tyr Glu Ala Met Asn Asn Ala Gly Tyr Leu Asp Ser Asp Met Ile
 225 230 235 240

5 Val Ile Leu Asn Asp Asn Arg Gln Val Ser Leu Pro Thr Ala Thr Leu
 245 250 255

10 Asp Gly Pro Val Ala Pro Val Gly Ala Leu Ser Ser Ala Leu Ser Arg
 260 265 270

15 Leu Gln Ser Asn Arg Pro Leu Arg Glu Leu Arg Glu Val Ala Lys Gly
 275 280 285

Val Thr Lys Gln Ile Gly Gly Pro Met His Glu Leu Ala Ala Lys Val
 290 295 300

20 Asp Glu Tyr Ala Arg Gly Met Ile Ser Gly Ser Gly Ser Thr Leu Phe
 305 310 315 320

25 Glu Glu Leu Gly Leu Tyr Tyr Ile Gly Pro Val Asp Gly His Asn Ile
 325 330 335

30 Asp Asp Leu Ile Ala Ile Leu Lys Glu Val Arg Ser Thr Lys Thr Thr
 340 345 350

35 Gly Pro Val Leu Ile His Val Val Thr Glu Lys Gly Arg Gly Tyr Pro
 355 360 365

Tyr Ala Glu Arg Ala Ala Asp Lys Tyr His Gly Val Ala Lys Phe Asp
 370 375 380

40 Pro Ala Thr Gly Lys Gln Phe Lys Ala Ser Ala Lys Thr Gln Ser Tyr
 385 390 395 400

45 Thr Thr Tyr Phe Ala Glu Ala Leu Ile Ala Glu Ala Glu Ala Asp Lys

175

405

410

415

5 Asp Ile Val Ala Ile His Ala Ala Met Gly Gly Gly Thr Gly Met Asn
420 425 430

10 Leu Phe His Arg Arg Phe Pro Thr Arg Cys Phe Asp Val Gly Ile Ala
435 440 445

15 Glu Gln His Ala Val Thr Phe Ala Ala Gly Leu Ala Cys Glu Gly Ile
450 455 460

Lys Pro Phe Cys Ala Ile Tyr Ser Ser Phe Met Gln Arg Ala Tyr Asp
465 470 475 480

20 Gln Val Val His Asp Val Asp Leu Gln Lys Leu Pro Val Arg Phe Ala
485 490 495

25 Met Asp Arg Ala Gly Leu Val Gly Ala Asp Gly Pro Thr His Cys Gly
500 505 510

30 Ala Phe Asp Val Thr Tyr Met Ala Cys Leu Pro Asn Met Val Val Met
515 520 525

Ala Pro Ser Asp Glu Ala Glu Leu Phe His Met Val Ala Thr Ala Ala
530 535 540

35 Ala Ile Asp Asp Arg Pro Ser Cys Phe Arg Tyr Pro Arg Gly Asn Gly
545 550 555 560

40 Ile Gly Val Glu Leu Pro Ala Gly Asn Lys Gly Ile Pro Leu Glu Val
565 570 575

45 Gly Lys Gly Arg Ile Leu Ile Glu Gly Glu Arg Val Ala Leu Leu Gly
580 585 590

5 Tyr Gly Ser Ala Val Gln Asn Cys Leu Asp Ala Ala Ile Val Leu Glu
595 600 605

10 Ser Arg Gly Leu Gln Val Thr Val Ala Asp Ala Arg Phe Cys Lys Pro
610 615 620

15 Leu Asp His Ala Leu Ile Arg Ser Leu Ala Lys Ser His Glu Val Leu
625 630 635 640

20 Ile Thr Val Glu Glu Gly Ser Ile Gly Gly Phe Gly Ser His Val Val
645 650 655

25 Gln Phe Met Ala Leu Asp Gly Leu Leu Asp Gly Lys Leu Lys Trp Arg
660 665 670

30 Pro Ile Val Leu Pro Asp Arg Tyr Ile Asp His Gly Ser Pro Val Asp
675 680 685

35 Gln Leu Ala Glu Ala Gly Leu Thr Pro Ser His Ile Ala Ala Thr Val
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ttc ttg gat acc tcc agg ttc aat cca atc cct aaa ctc tca ggt ggg 96

Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly

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ttt agt ttg agg agg agg aat caa ggg aga ggt ttt gga aaa ggt gtt 144

Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val

35 40 45

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aag tgt tca gtg aaa gtg cag cag caa caa caa cct cct cca gca tgg 192

Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp

50 55 60

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cct ggg aga gct gtc cct gag gcg cct cgt caa tct tgg gat gga cca 240

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro

65 70 75 80

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aaa ccc atc tct atc gtt gga tct act ggt tct att ggc act cag aca 288

Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr

85 90 95

ttg gat att gtg gct gag aat cct gac aaa ttc aga gtt gtg gct cta 336

Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu

100 105 110

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gct gct ggt tcg aat gtt act cta ctt gct gat cag gta agg aga ttt 384

Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe

115 120 125

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aag cct gca ttg gtt gct gtt aga aac gag tca ctg att aat gag ctt 432

Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu

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	Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly			
5	145	150	155	160
	gag caa gga gtg att gag gtt gcc cga cat cct gaa gct gta acc gtt			528
	Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val			
		165	170	175
10	gtt acc gga ata gta ggt tgt gcg gga cta aag cct acg gtt gct gca			576
	Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala			
		180	185	190
15	att gaa gca gga aag gac att gct ctt gca aac aaa gag aca tta atc			624
	Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile			
		195	200	205
	gca ggt ggt cct ttc gtg ctt ccg ctt gcc aac aaa cat aat gta aag			672
20	Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys			
		210	215	220
	att ctt ccg gca gat tca gaa cat tct gcc ata ttt cag tgt att caa			720
	Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln			
25	225	230	235	240
	ggg ttg cct gaa ggc gct ctg cgc aag ata atc ttg act gca tct ggt			768
	Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly			
		245	250	255
30	gga gct ttt agg gat tgg cct gtc gaa aag cta aag gaa gtt aaa gta			816
	Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val			
		260	265	270
35	gcg gat gcg ttg aag cat cca aac tgg aac atg gga aag aaa atc act			864
	Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr			
		275	280	285
	gtg gac tct gct acg ctt ttc aac aag ggt ctt gag gtc att gaa gcg			912
40	Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala			
		290	295	300
	cat tat ttg ttt gga gct gag tat gac gat ata gag att gtc att cat			960
	His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His			
45	305	310	315	320

ccg caa agt atc ata cat tcc atg att gaa aca cag gat tca tct gtg 1008
 Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

5 ctt gct caa ttg ggt tgg cct gat atg cgt tta ccg att ctc tac acc 1056
 Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

10 atg tca tgg ccc gat aga gtt cct tgt tct gaa gta act tgg cca aga 1104
 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

15 ctt gac ctt tgc aaa ctc ggt tca ttg act ttc aag aaa cca gac aat 1152
 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

20 gtg aaa tac cca tcc atg gat ctt gct tat gct gct gga cga gct gga 1200
 Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
 385 390 395 400

ggc aca atg act gga gtt ctc agc gcc gcc aat gag aaa gct gtt gaa 1248
 Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

25 atg ttc att gat gaa aag ata agc tat ttg gat atc ttc aag gtt gtg 1296
 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
 420 425 430

30 gaa tta aca tgc gat aaa cat cga aac gag ttg gta aca tca ccg tct 1344
 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
 435 440 445

35 ctt gaa gag att gtt cac tat gac ttg tgg gca cgt gaa tat gcc gcg 1392
 Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
 450 455 460

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Phe Leu Asp Thr Ser Arg Phe Asn Pro Ile Pro Lys Leu Ser Gly Gly
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Phe Ser Leu Arg Arg Arg Asn Gln Gly Arg Gly Phe Gly Lys Gly Val
 35 40 45

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Lys Cys Ser Val Lys Val Gln Gln Gln Gln Gln Pro Pro Pro Ala Trp
 50 55 60

Pro Gly Arg Ala Val Pro Glu Ala Pro Arg Gln Ser Trp Asp Gly Pro
 65 70 75 80

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Lys Pro Ile Ser Ile Val Gly Ser Thr Gly Ser Ile Gly Thr Gln Thr
 85 90 95

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Leu Asp Ile Val Ala Glu Asn Pro Asp Lys Phe Arg Val Val Ala Leu
 100 105 110

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Ala Ala Gly Ser Asn Val Thr Leu Leu Ala Asp Gln Val Arg Arg Phe
 115 120 125

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Lys Pro Ala Leu Val Ala Val Arg Asn Glu Ser Leu Ile Asn Glu Leu
 130 135 140

Lys Glu Ala Leu Ala Asp Leu Asp Tyr Lys Leu Glu Ile Ile Pro Gly
 145 150 155 160

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Glu Gln Gly Val Ile Glu Val Ala Arg His Pro Glu Ala Val Thr Val
 165 170 175

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Val Thr Gly Ile Val Gly Cys Ala Gly Leu Lys Pro Thr Val Ala Ala
 180 185 190

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Ile Glu Ala Gly Lys Asp Ile Ala Leu Ala Asn Lys Glu Thr Leu Ile
 195 200 205

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Ala Gly Gly Pro Phe Val Leu Pro Leu Ala Asn Lys His Asn Val Lys
 210 215 220

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Ile Leu Pro Ala Asp Ser Glu His Ser Ala Ile Phe Gln Cys Ile Gln
 225 230 235 240

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Gly Leu Pro Glu Gly Ala Leu Arg Lys Ile Ile Leu Thr Ala Ser Gly
 245 250 255

35

Gly Ala Phe Arg Asp Trp Pro Val Glu Lys Leu Lys Glu Val Lys Val
 260 265 270

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Ala Asp Ala Leu Lys His Pro Asn Trp Asn Met Gly Lys Lys Ile Thr
 275 280 285

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Val Asp Ser Ala Thr Leu Phe Asn Lys Gly Leu Glu Val Ile Glu Ala
 290 295 300

His Tyr Leu Phe Gly Ala Glu Tyr Asp Asp Ile Glu Ile Val Ile His
 305 310 315 320

182

Pro Gln Ser Ile Ile His Ser Met Ile Glu Thr Gln Asp Ser Ser Val
 325 330 335

5 Leu Ala Gln Leu Gly Trp Pro Asp Met Arg Leu Pro Ile Leu Tyr Thr
 340 345 350

10 Met Ser Trp Pro Asp Arg Val Pro Cys Ser Glu Val Thr Trp Pro Arg
 355 360 365

15 Leu Asp Leu Cys Lys Leu Gly Ser Leu Thr Phe Lys Lys Pro Asp Asn
 370 375 380

Val Lys Tyr Pro Ser Met Asp Leu Ala Tyr Ala Ala Gly Arg Ala Gly
 385 390 395 400

20 Gly Thr Met Thr Gly Val Leu Ser Ala Ala Asn Glu Lys Ala Val Glu
 405 410 415

25 Met Phe Ile Asp Glu Lys Ile Ser Tyr Leu Asp Ile Phe Lys Val Val
 420 425 430

30 Glu Leu Thr Cys Asp Lys His Arg Asn Glu Leu Val Thr Ser Pro Ser
 435 440 445

35 Leu Glu Glu Ile Val His Tyr Asp Leu Trp Ala Arg Glu Tyr Ala Ala
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cttccatcac taacagtcct cgccgaggggt tgaatcgggt gttcgcctca acgtcgact 179

atg ggt gaa gtc gct gat gct ggt atg gat gcc gtc cag aag cgg ctt 227

25 Met Gly Glu Val Ala Asp Ala Gly Met Asp Ala Val Gln Lys Arg Leu
1 5 10 15atg ttc gac gat gaa tgt att ttg gtg gat gag aat gac aag gtc gtc 275
Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val

30 20 25 30

gga cat gat tcc aaa tac aac tgt cat ttg atg gaa aag ata gag gca 323
Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
35 40 45

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gaa aac ttg ctt cac aga gcc ttc agt gtt ttc tta ttc aac tca aaa 371
Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
50 55 60

40 tac gag ttg ctt ctt cag caa cga tct gca acg aag gta aca ttc ccg 419

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
65 70 75 80

ctc gta tgg aca aac acc tgt tgc agc cat ccc ctc ttc cgt gat tcc 467

45 Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser

5 gaa ctc ata gaa gaa aat ttt ctc ggg gta cga aac gct gca caa agg 515
 Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110

10 aag ctt tta gac gag cta ggc att cca gct gaa gac gta cca gtt gat 563
 Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125

15 gaa ttc act cct ctt ggt cgc att ctt tao aaa gct cca tct gac gga 611
 Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140

20 aaa tgg gga gag cac gaa ctg gac tat ctt ctg ttt att gtc cga gat 659
 Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160

25 gtg aaa tac gat cca aac cca gat gaa gtt gct gac gct aag tac gtt 707
 Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175

30 aat cgc gag gag ttg aaa gag ata ctg aga aaa gct gat gca ggt gaa 755
 Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190

35 gag gga ata aag ttg tct cct tgg ttt aga ttg gtt gtg gat aac ttt 803
 Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
 195 200 205

40 ttg ttc aag tgg tgg gat cat gta gag gag ggg aag att aag gac gtc 851
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45 gcc gac atg aaa act atc cac aag ttg act taa 884
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<213> Adonis palaestina clone ApIP128

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Met Phe Asp Asp Glu Cys Ile Leu Val Asp Glu Asn Asp Lys Val Val
 20 25 30

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Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Lys Ile Glu Ala
 35 40 45

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Glu Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe Asn Ser Lys
 50 55 60

25

Tyr Glu Leu Leu Leu Gln Gln Arg Ser Ala Thr Lys Val Thr Phe Pro
 65 70 75 80

Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Phe Arg Asp Ser
 85 90 95

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Glu Leu Ile Glu Glu Asn Phe Leu Gly Val Arg Asn Ala Ala Gln Arg
 100 105 110

35

Lys Leu Leu Asp Glu Leu Gly Ile Pro Ala Glu Asp Val Pro Val Asp
 115 120 125

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Glu Phe Thr Pro Leu Gly Arg Ile Leu Tyr Lys Ala Pro Ser Asp Gly
 130 135 140

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Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile Val Arg Asp
 145 150 155 160

186

Val Lys Tyr Asp Pro Asn Pro Asp Glu Val Ala Asp Ala Lys Tyr Val
 165 170 175

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Asn Arg Glu Glu Leu Lys Glu Ile Leu Arg Lys Ala Asp Ala Gly Glu
 180 185 190

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Glu Gly Ile Lys Leu Ser Pro Trp Phe Arg Leu Val Val Asp Asn Phe
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Leu Phe Lys Trp Trp Asp His Val Glu Glu Gly Lys Ile Lys Asp Val
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 Met Leu

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	Ser Phe Tyr Gly Ser Ser Gln Ser Leu Ala Ser His Arg Phe Ala Ile	
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	att ccc gat cag ggt cac tct tgt tct gac tct cca cac aag ggt tac	201
	Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys Gly Tyr	
	35 40 45 50	
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	gtt tgc aga aca act tat tca ttg aaa tct ccg gtt ttt ggt gga ttt	249
	Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly Gly Phe	
	55 60 65	
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	agt cat caa ctc tat cac cag agt agc tcc ttg gtt gag gag gag ctt	297
	Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu Glu Leu	
	70 75 80	
25		
	gac cca ttt tcg ctt gtt gcc gat gag ctg tca ctt ctt agt aat aag	345
	Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser Asn Lys	
	85 90 95	
30		
	ttg aga gag atg gta ctt gcc gag gtt cca aag ctt gcc tct gct gct	393
	Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser Ala Ala	
	100 105 110	
35		
	gag tac ttc ttc aaa agg ggt gtg caa gga aaa cag ttt cgt tca act	441
	Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg Ser Thr	
	115 120 125 130	
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	att ttg ctg ctg atg gcg aca gct ctg gat gta cga gtt cca gaa gca	489
	Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro Glu Ala	
	135 140 145	
45		
	ttg att ggg gaa tca aca gat ata gtc aca tca gaa tta cgc gta agg	537
	Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg Val Arg	
	150 155 160	
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	caa cgg ggt att gct gaa atc act gaa atg ata cac gtc gca agt cta	585
	Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala Ser Leu	
	165 170 175	

188

	ctg cac gat gat gtc ttg gat gat gcc gat aca agg cgt ggt gtt ggt	633
	Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly Val Gly	
	180 185 190	
5	tcc tta aat gtt gta atg ggt aac aag atg tcg gta tta gca gga gac	681
	Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala Gly Asp	
	195 200 205 210	
	ttc ttg ctc tcc cgg gct tgt ggg gct ctc gct gct tta aag aac aca	729
10	Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys Asn Thr	
	215 220 225	
	gag gtt gta gca tta ctt gca act gct gta gaa cat ctt gtt acc ggt	777
15	Glu Val Val Ala Leu Leu Ala Thr Ala Val Glu His Leu Val Thr Gly	
	230 235 240	
	gaa acc atg gag ata act agt tca acc gag cag cgt tat agt atg gac	825
	Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser Met Asp	
	245 250 255	
20	tac tac atg cag aag aca tat tat aag aca gca tcg cta atc tct aac	873
	Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile Ser Asn	
	260 265 270	
25	agc tgc aaa gct gtt gcc gtt ctc act gga caa aca gca gaa gtt gcc	921
	Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu Val Ala	
	275 280 285 290	
	gtg tta gct ttt gag tat ggg agg aat ctg ggt tta gca ttc caa tta	969
30	Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Leu	
	295 300 305	
	ata gac gac att ctt gat ttc acg ggc aca tct gcc tct ctc gga aag	1017
	Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu Gly Lys	
35	310 315 320	
	gga tcg ttg tca gat att cgc cat gga gtc ata aca gcc cca atc ctc	1065
	Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro Ile Leu	
	325 330 335	
40	ttt gcc atg gaa gag ttt cct caa cta cgc gaa gtt gtt gat caa gtt	1113
	Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp Gln Val	
	340 345 350	
45	gaa aaa gat cct agg aat gtt gac att gct tta gag tat ctt ggg aag	1161

189

Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu Gly Lys
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5 agc aag gga ata cag agg gca aga gaa tta gcc atg gaa cat gcg aat 1209
 Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His Ala Asn
 375 380 385

10 cta gca gca gct gca atc ggg tct cta cct gaa aca gac aat gaa gat 1257
 Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn Glu Asp
 390 395 400

15 gtc aaa aga tcg agg cgg gca ctt att gac ttg acc cat aga gtc atc 1305
 Val Lys Arg Ser Arg Arg Ala Leu Ile Asp Leu Thr His Arg Val Ile
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acc aga aac aag tgagattaag taatgtttct ctctatacac caaaacattc 1357
 Thr Arg Asn Lys
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45 Ala Ile Ile Pro Asp Gln Gly His Ser Cys Ser Asp Ser Pro His Lys
 35 40 45

190

Gly Tyr Val Cys Arg Thr Thr Tyr Ser Leu Lys Ser Pro Val Phe Gly
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5

Gly Phe Ser His Gln Leu Tyr His Gln Ser Ser Ser Leu Val Glu Glu
 65 70 75 80

10

Glu Leu Asp Pro Phe Ser Leu Val Ala Asp Glu Leu Ser Leu Leu Ser
 85 90 95

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Asn Lys Leu Arg Glu Met Val Leu Ala Glu Val Pro Lys Leu Ala Ser
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Ala Ala Glu Tyr Phe Phe Lys Arg Gly Val Gln Gly Lys Gln Phe Arg
 115 120 125

Ser Thr Ile Leu Leu Leu Met Ala Thr Ala Leu Asp Val Arg Val Pro
 130 135 140

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Glu Ala Leu Ile Gly Glu Ser Thr Asp Ile Val Thr Ser Glu Leu Arg
 145 150 155 160

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Val Arg Gln Arg Gly Ile Ala Glu Ile Thr Glu Met Ile His Val Ala
 165 170 175

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Ser Leu Leu His Asp Asp Val Leu Asp Asp Ala Asp Thr Arg Arg Gly
 180 185 190

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Val Gly Ser Leu Asn Val Val Met Gly Asn Lys Met Ser Val Leu Ala
 195 200 205

Gly Asp Phe Leu Leu Ser Arg Ala Cys Gly Ala Leu Ala Ala Leu Lys
 210 215 220

45

191

Asn	Thr	Glu	Val	Val	Ala	Leu	Leu	Ala	Thr	Ala	Val	Glu	His	Leu	Val
225					230					235					240

5 Thr Gly Glu Thr Met Glu Ile Thr Ser Ser Thr Glu Gln Arg Tyr Ser
245 250 255

Met Asp Tyr Tyr Met Gln Lys Thr Tyr Tyr Lys Thr Ala Ser Leu Ile
10 260 265 270

Ser Asn Ser Cys Lys Ala Val Ala Val Leu Thr Gly Gln Thr Ala Glu
275 280 285

Val Ala Val Leu Ala Phe Glu Tyr Gly Arg Asn Leu Gly Leu Ala Phe
290 295 300

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Gln Leu Ile Asp Asp Ile Leu Asp Phe Thr Gly Thr Ser Ala Ser Leu

305 310 315 320

25 Gly Lys Gly Ser Leu Ser Asp Ile Arg His Gly Val Ile Thr Ala Pro
325 330 335

Ile Leu Phe Ala Met Glu Glu Phe Pro Gln Leu Arg Glu Val Val Asp
30 340 345 350

Gln Val Glu Lys Asp Pro Arg Asn Val Asp Ile Ala Leu Glu Tyr Leu
355 360 365

Gly Lys Ser Lys Gly Ile Gln Arg Ala Arg Glu Leu Ala Met Glu His
370 375 380

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Ala Asn Leu Ala Ala Ala Ala Ile Gly Ser Leu Pro Glu Thr Asp Asn
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gca ata cct tca cat cat ttg cat ctg aga agt ctt ggt ggg agt ctc

96

Ala Ile Pro Ser His His Leu His Leu Arg Ser Leu Gly Gly Ser Leu

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25

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tat cgt cgt cgt atc caa agc tct tca atg gag acc gat ctc aag tca

144

Tyr Arg Arg Arg Ile Gln Ser Ser Ser Met Glu Thr Asp Leu Lys Ser

35

40

45

40

acc ttt ctc aac gtt tat tct gtt ctc aag tct gac ctt ctt cat gac

192

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp

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55

60

45

cct tcc ttc gaa ttc acc aat gaa tct cgt ctc tgg gtt gat cgg atg

240

193

	Pro	Ser	Phe	Glu	Phe	Thr	Asn	Glu	Ser	Arg	Leu	Trp	Val	Asp	Arg	Met	
	65					70					75					80	
5	ctg	gac	tac	aat	gta	cgt	gga	ggg	aaa	ctc	aat	cgg	ggg	ctc	tct	ggt	288
	Leu	Asp	Tyr	Asn	Val	Arg	Gly	Gly	Lys	Leu	Asn	Arg	Gly	Leu	Ser	Val	
					85					90				95			
10	ggt	gac	agt	ttc	aaa	ctt	ttg	aag	caa	ggc	aat	gat	ttg	act	gag	caa	336
	Val	Asp	Ser	Phe	Lys	Leu	Leu	Lys	Gln	Gly	Asn	Asp	Leu	Thr	Glu	Gln	
				100					105					110			
15	gag	ggt	ttc	ctc	tct	tgt	gct	ctc	ggg	tgg	tgc	att	gaa	tgg	ctc	caa	384
	Glu	Val	Phe	Leu	Ser	Cys	Ala	Leu	Gly	Trp	Cys	Ile	Glu	Trp	Leu	Gln	
			115					120					125				
20	gct	tat	ttc	ctt	gtg	ctt	gat	gat	att	atg	gat	aac	tct	gtc	act	cgc	432
	Ala	Tyr	Phe	Leu	Val	Leu	Asp	Asp	Ile	Met	Asp	Asn	Ser	Val	Thr	Arg	
		130					135				140						
25	cgt	ggg	caa	cct	tgc	tgg	ttc	aga	ggt	cct	cag	ggt	ggg	atg	ggt	gcc	480
	Arg	Gly	Gln	Pro	Cys	Trp	Phe	Arg	Val	Pro	Gln	Val	Gly	Met	Val	Ala	
	145				150					155				160			
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	Ile	Asn	Asp	Gly	Ile	Leu	Leu	Arg	Asn	His	Ile	His	Arg	Ile	Leu	Lys	
				165					170					175			
35	aag	cat	ttc	cgt	gat	aag	cct	tac	tat	ggt	gac	ctt	ggt	gat	ttg	ttt	576
	Lys	His	Phe	Arg	Asp	Lys	Pro	Tyr	Tyr	Val	Asp	Leu	Val	Asp	Leu	Phe	
			180					185						190			
40	aat	gag	ggt	gag	ttg	caa	aca	gct	tgt	ggc	cag	atg	ata	gat	ttg	atc	624
	Asn	Glu	Val	Glu	Leu	Gln	Thr	Ala	Cys	Gly	Gln	Met	Ile	Asp	Leu	Ile	
		195					200					205					
45	acc	acc	ttt	gaa	gga	gaa	aag	gat	ttg	gcc	aag	tac	tca	ttg	tca	atc	672
	Thr	Thr	Phe	Glu	Gly	Glu	Lys	Asp	Leu	Ala	Lys	Tyr	Ser	Leu	Ser	Ile	
		210					215					220					
50	cac	cgt	cgt	att	gtc	cag	tac	aaa	acg	gct	tat	tac	tca	ttt	tat	ctc	720
	His	Arg	Arg	Ile	Val	Gln	Tyr	Lys	Thr	Ala	Tyr	Tyr	Ser	Phe	Tyr	Leu	
	225				230					235						240	
55	cct	ggt	gct	tgt	gcg	ttg	ctt	atg	gcg	ggc	gaa	aat	ttg	gaa	aac	cat	768
	Pro	Val	Ala	Cys	Ala	Leu	Leu	Met	Ala	Gly	Glu	Asn	Leu	Glu	Asn	His	

194

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	Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val			
5	260	265	270	
	cag gat gat tat ctg gat tgt ttt gct gat ccc gag acg ctt ggc aag			864
	Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys			
	275	280	285	
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	ata gga aca gat ata gaa gat ttc aaa tgc tcg tgg ttg gtg gtt aag			912
	Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys			
	290	295	300	
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	gca tta gag cgc tgc agc gaa gaa caa act aag ata tta tat gag aac			960
	Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn			
	305	310	315	320
	tat ggt aaa ccc gac cca tcg aac gtt gct aaa gtg aag gat ctc tac			1008
20	Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr			
	325	330	335	
	aaa gag ctg gat ctt gag gga gtt ttc atg gag tat gag agc aaa agc			1056
	Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser			
25	340	345	350	
	tac gag aag ctg act gga gcg att gag gga cac caa agt aaa gca atc			1104
	Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile			
	355	360	365	
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	caa gca gtg cta aaa tcc ttc ttg gct aag atc tac aag agg cag aag			1152
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35 40 45

Thr Phe Leu Asn Val Tyr Ser Val Leu Lys Ser Asp Leu Leu His Asp
50 55 60

20 Pro Ser Phe Glu Phe Thr Asn Glu Ser Arg Leu Trp Val Asp Arg Met
65 70 75 80

25 Leu Asp Tyr Asn Val Arg Gly Gly Lys Leu Asn Arg Gly Leu Ser Val
85 90 95

30 Val Asp Ser Phe Lys Leu Leu Lys Gln Gly Asn Asp Leu Thr Glu Gln
100 105 110

35 Glu Val Phe Leu Ser Cys Ala Leu Gly Trp Cys Ile Glu Trp Leu Gln
115 120 125

Ala Tyr Phe Leu Val Leu Asp Asp Ile Met Asp Asn Ser Val Thr Arg
130 135 140

40 Arg Gly Gln Pro Cys Trp Phe Arg Val Pro Gln Val Gly Met Val Ala
145 150 155 160

45 Ile Asn Asp Gly Ile Leu Leu Arg Asn His Ile His Arg Ile Leu Lys

5 Lys His Phe Arg Asp Lys Pro Tyr Tyr Val Asp Leu Val Asp Leu Phe
 180 185 190

10 Asn Glu Val Glu Leu Gln Thr Ala Cys Gly Gln Met Ile Asp Leu Ile
 195 200 205

15 Thr Thr Phe Glu Gly Glu Lys Asp Leu Ala Lys Tyr Ser Leu Ser Ile
 210 215 220

20 His Arg Arg Ile Val Gln Tyr Lys Thr Ala Tyr Tyr Ser Phe Tyr Leu
 225 230 235 240

25 Ile Asp Val Lys Asn Val Leu Val Asp Met Gly Ile Tyr Phe Gln Val
 260 265 270

30 Gln Asp Asp Tyr Leu Asp Cys Phe Ala Asp Pro Glu Thr Leu Gly Lys
 275 280 285

35 Ile Gly Thr Asp Ile Glu Asp Phe Lys Cys Ser Trp Leu Val Val Lys
 290 295 300

40 Ala Leu Glu Arg Cys Ser Glu Glu Gln Thr Lys Ile Leu Tyr Glu Asn
 305 310 315 320

45 Tyr Gly Lys Pro Asp Pro Ser Asn Val Ala Lys Val Lys Asp Leu Tyr
 325 330 335

Lys Glu Leu Asp Leu Glu Gly Val Phe Met Glu Tyr Glu Ser Lys Ser
 340 345 350

Tyr Glu Lys Leu Thr Gly Ala Ile Glu Gly His Gln Ser Lys Ala Ile
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 cat cct tca act atc tta acc caa tcc aga tcc aga tct cct cct tct 96
 His Pro Ser Thr Ile Leu Thr Gln Ser Arg Ser Arg Ser Pro Pro Ser
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 ctc atc acc ctt aaa ccc atc tcc ctc act cca aaa cgc acc gtt tcg 144
 Leu Ile Thr Leu Lys Pro Ile Ser Leu Thr Pro Lys Arg Thr Val Ser
 35 40 45

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 tct tct tcc tcc tct tcc ctc atc acc aaa gaa gac aac aac ctc aaa 192
 Ser Ser Ser Ser Ser Ser Leu Ile Thr Lys Glu Asp Asn Asn Leu Lys

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	Ser Ser Ser Ser Ser Phe Asp Phe Met Ser Tyr Ile Ile Arg Lys Ala					
5	65		70		75	80
	gac tcc gtc aac aaa gcc tta gac tcc gcc gtc cct ctc cgg gag cca					288
	Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro					
		85		90		95
10	ctc aag atc cac gaa gcg atg cgt tac tct ctc ctc gcc gga gga aaa					336
	Leu Lys Ile His Glu Ala Met Arg Tyr Ser Leu Leu Ala Gly Gly Lys					
		100		105		110
15	cgc gtc aga cca gtt ctc tgc atc gcc gcg tgc gag cta gtc gga gga					384
	Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly					
		115		120		125
	gaa gag tct tta gct atg ccg gcg cgt tgc gcc gtg gaa atg atc cac					432
20	Glu Glu Ser Leu Ala Met Pro Ala Arg Cys Ala Val Glu Met Ile His					
		130		135		140
	acc atg tcg ttg atc cac gac gac ttg cct tgt atg gat aac gac gat					480
	Thr Met Ser Leu Ile His Asp Asp Leu Pro Cys Met Asp Asn Asp Asp					
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	ctc cgc cgc gga aag ccc acg aat cac aaa gtt tac ggc gaa gac gtg					528
	Leu Arg Arg Gly Lys Pro Thr Asn His Lys Val Tyr Gly Glu Asp Val					
		165		170		175
30	gcg gtt tta gcc gga gac gcg ctt ctt tcg ttc gcc ttc gag cat tta					576
	Ala Val Leu Ala Gly Asp Ala Leu Leu Ser Phe Ala Phe Glu His Leu					
		180		185		190
35	gcg tcg gct acg agc tcg gag gtt tct ccg gcg aga gtg gtt aga gct					624
	Ala Ser Ala Thr Ser Ser Glu Val Ser Pro Ala Arg Val Val Arg Ala					
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	gtg gga gag ttg gct aaa gcc atc ggc acc gaa ggg ctc gtg gcg gga					672
40	Val Gly Glu Leu Ala Lys Ala Ile Gly Thr Glu Gly Leu Val Ala Gly					
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	caa gtg gtg gat ata agc agt gaa ggg ttg gac tta aac aac gtc gga					720
	Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly					
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	gaa gct tca gcg gtt ttg ggt ggg atc atc ggt gga ggg agt gat gaa	816
	Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
	260 265 270	
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	Glu Ile Glu Arg Leu Arg Lys Phe Ala Arg Cys Ile Gly Leu Leu Phe	
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	Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
	290 295 300	
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	ggg aaa acc gct ggg aaa gat ttg att gct gat aag ttg act tat ccg	960
	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
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	Lys Leu Met Gly Leu Glu Lys Ser Arg Glu Phe Ala Glu Lys Leu Asn	
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	cct ttg ttg gct ttg gct aat tac att gcc aat aga cag aac tga	1101
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 Asp Ser Val Asn Lys Ala Leu Asp Ser Ala Val Pro Leu Arg Glu Pro
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 Arg Val Arg Pro Val Leu Cys Ile Ala Ala Cys Glu Leu Val Gly Gly
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 165 170 175
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201

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	210	215 220
15	Gln Val Val Asp Ile Ser Ser Glu Gly Leu Asp Leu Asn Asn Val Gly	
	225	230 235 240
20	Leu Glu His Leu Lys Phe Ile His Leu His Lys Thr Ala Ala Leu Leu	
	245	250 255
25	Glu Ala Ser Ala Val Leu Gly Gly Ile Ile Gly Gly Gly Ser Asp Glu	
	260	265 270
30	Gln Val Val Asp Asp Ile Leu Asp Val Thr Lys Ser Ser Gln Glu Leu	
	290	295 300
35	Gly Lys Thr Ala Gly Lys Asp Leu Ile Ala Asp Lys Leu Thr Tyr Pro	
	305	310 315 320
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	325	330 335
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	ggc tcg aaa agt ttt gcg aca gcc tca aag tta ttt gat gca aaa acc			96
30	Gly Ser Lys Ser Phe Ala Thr Ala Ser Lys Leu Phe Asp Ala Lys Thr			
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	Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp			
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	Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu			
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40	caa acg ccc gaa caa cgt ctg atg caa ctt gag atg aaa acg cgc cag			240
	Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln			
	65 70 75 80			
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	Ala Tyr Ala Gly Ser Gln Met His Glu Pro Ala Phe Ala Ala Phe Gln	
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	100 105 110	
10	ctg gaa ggc ttc gcc atg gat gta cgc gaa gcg caa tac agc caa ctg Leu Glu Gly Phe Ala Met Asp Val Arg Glu Ala Gln Tyr Ser Gln Leu	384
	115 120 125	
15	gat gat acc ctg cgc tat tgc tat cac gtt gca ggc gtt gtc ggc ttg Asp Asp Thr Leu Arg Tyr Cys Tyr His Val Ala Gly Val Val Gly Leu	432
	130 135 140	
	atg atg gcg caa atc atg ggc gtg cgg gat aac gcc acc ctg gac cgc Met Met Ala Gln Ile Met Gly Val Arg Asp Asn Ala Thr Leu Asp Arg	480
	145 150 155 160	
20	gcc tgt gac ctt ggg ctg gca ttt cag ttg acc aat att gct cgc gat Ala Cys Asp Leu Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp	528
	165 170 175	
25	att gtg gac gat gcg cat gcg ggc cgc tgt tat ctg ccg gca agc tgg Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp	576
	180 185 190	
30	ctg gag cat gaa ggt ctg aac aaa gag aat tat gcg gca cct gaa aac Leu Glu His Glu Gly Leu Asn Lys Glu Asn Tyr Ala Ala Pro Glu Asn	624
	195 200 205	
35	cgt cag gcg ctg agc cgt atc gcc cgt cgt ttg gtg cag gaa gca gaa Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu	672
	210 215 220	
	cct tac tat ttg tct gcc aca gcc ggc ctg gca ggg ttg ccc ctg cgt Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg	720
	225 230 235 240	
40	tcc gcc tgg gca atc gct acc gcg aag cag gtt tac ccg aaa ata ggt Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly	768
	245 250 255	
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204

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	Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln			
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	gcc ctt act tcc cgg atg cgg gct cat cct ccc cgc cct gcg cat ctc			912
	Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu			
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	Trp Gln Arg Pro Leu			
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35	Arg Arg Ser Val Leu Met Leu Tyr Ala Trp Cys Arg His Cys Asp Asp			
	35 40 45			
40	Val Ile Asp Asp Gln Thr Leu Gly Phe Gln Ala Arg Gln Pro Ala Leu			
	50 55 60			
45	Gln Thr Pro Glu Gln Arg Leu Met Gln Leu Glu Met Lys Thr Arg Gln			
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 Glu Val Ala Met Ala His Asp Ile Ala Pro Ala Tyr Ala Phe Asp His
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 165 170 175
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 Ile Val Asp Asp Ala His Ala Gly Arg Cys Tyr Leu Pro Ala Ser Trp
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 Arg Gln Ala Leu Ser Arg Ile Ala Arg Arg Leu Val Gln Glu Ala Glu
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 Pro Tyr Tyr Leu Ser Ala Thr Ala Gly Leu Ala Gly Leu Pro Leu Arg
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 Ser Ala Trp Ala Ile Ala Thr Ala Lys Gln Val Tyr Arg Lys Ile Gly
 245 250 255
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Val Lys Val Glu Gln Ala Gly Gln Gln Ala Trp Asp Gln Arg Gln Ser
 260 265 270

5 Thr Thr Thr Pro Glu Lys Leu Thr Leu Leu Leu Ala Ala Ser Gly Gln
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10 Ala Leu Thr Ser Arg Met Arg Ala His Pro Pro Arg Pro Ala His Leu
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gca att cgt cta caa gct gcg ggg atc ccc gtc tta ctg ctt gaa caa 96
 45 Ala Ile Arg Leu Gln Ala Ala Gly Ile Pro Val Leu Leu Leu Glu Gln
 20 25 30

5 cgt gat aaa ccc ggc ggt cgg gct tat gtc tac gag gat cag ggg ttt 144
 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
 35 40 45
 acc ttt gat gca ggc ccg acg gtt atc acc gat ccc agt gcc att gaa 192
 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
 50 55 60
 10 gaa ctg ttt gca ctg gca gga aaa cag tta aaa gag tat gtc gaa ctg 240
 Glu Leu Phe Ala Leu Ala Gly Lys Gln Leu Lys Glu Tyr Val Glu Leu
 65 70 75 80
 15 ctg ccg gtt acg ccg ttt tac cgc ctg tgt tgg gag tca ggg aag gtc 288
 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95
 20 ttt aat tac gat aac gat caa acc cgg ctc gaa gcg cag att cag cag 336
 Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
 100 105 110
 ttt aat ccc cgc gat gtc gaa ggt tat cgt cag ttt ctg gac tat tca 384
 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125
 25 cgc gcg gtg ttt aaa gaa ggc tat cta aag ctc ggt act gtc cct ttt 432
 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
 130 135 140
 30 tta tcg ttc aga gac atg ctt cgc gcc gca cct caa ctg gcg aaa ctg 480
 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160
 35 cag gca tgg aga agc gtt tac agt aag gtt gcc agt tac atc gaa gat 528
 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175
 40 gaa cat ctg cgc cag gcg ttt tct ttc cac tcg ctg ttg gtg ggc ggc 576
 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190
 aat ccc ttc gcc acc tca tcc att tat acg ttg ata cac gcg ctg gag 624
 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205
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208

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	Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu	
	225 230 235 240	
	aac gcc aga gtc agc cat atg gaa acg aca gga aac aag att gaa gcc	768
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	245 250 255	
	gtg cat tta gag gac ggt cgc agg ttc ctg acg caa gcc gtc gcg tca	816
	Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser	
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	Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro	
	275 280 285	
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	Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn	
	290 295 300	
25	tct ctg ttt gtg ctc tat ttt ggt ttg aat cac cat cat gat cag ctc	960
	Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu	
	305 310 315 320	
	gcg cat cac acg gtt tgt ttc ggc ccg cgt tac cgc gag ctg att gac	1008
30	Ala His His Thr Val Cys Phe Gly Pro Arg Tyr Arg Glu Leu Ile Asp	
	325 330 335	
	gaa att ttt aat cat gat ggc ctc gca gag gac ttc tca ctt tat ctg	1056
	Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu	
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	His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly	
	355 360 365	
40	agt tac tat gtg ttg gcg ccg gtg ccg cat tta ggc acc gcg aac ctc	1152
	Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu	
	370 375 380	
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209

	Asp	Trp	Thr	Val	Glu	Gly	Pro	Lys	Leu	Arg	Asp	Arg	Ile	Phe	Ala	Tyr	
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	Leu	Glu	Gln	His	Tyr	Met	Pro	Gly	Leu	Arg	Ser	Gln	Leu	Val	Thr	His	
					405					410					415		
10	cgg	atg	ttt	acg	ccg	ttt	gat	ttt	cgc	gac	cag	ctt	aat	gcc	tat	cat	1296
	Arg	Met	Phe	Thr	Pro	Phe	Asp	Phe	Arg	Asp	Gln	Leu	Asn	Ala	Tyr	His	
				420					425					430			
15	ggc	tca	gcc	ttt	tct	gtg	gag	ccc	gtt	ctt	acc	cag	agc	gcc	tgg	ttt	1344
	Gly	Ser	Ala	Phe	Ser	Val	Glu	Pro	Val	Leu	Thr	Gln	Ser	Ala	Trp	Phe	
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	Arg	Pro	His	Asn	Arg	Asp	Lys	Thr	Ile	Thr	Asn	Leu	Tyr	Leu	Val	Gly	
		450					455					460					
25	gca	ggc	acg	cat	ccc	ggc	gca	ggc	att	cct	ggc	gtc	atc	ggc	tcg	gca	1440
	Ala	Gly	Thr	His	Pro	Gly	Ala	Gly	Ile	Pro	Gly	Val	Ile	Gly	Ser	Ala	
	465					470					475				480		
30	aaa	gcg	aca	gca	ggt	ttg	atg	ctg	gag	gat	ctg	ata	tga				1479
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25

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5 Arg Asp Lys Pro Gly Gly Arg Ala Tyr Val Tyr Glu Asp Gln Gly Phe
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10 Thr Phe Asp Ala Gly Pro Thr Val Ile Thr Asp Pro Ser Ala Ile Glu
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 65 70 75 80

20 Leu Pro Val Thr Pro Phe Tyr Arg Leu Cys Trp Glu Ser Gly Lys Val
 85 90 95

25 Phe Asn Tyr Asp Asn Asp Gln Thr Arg Leu Glu Ala Gln Ile Gln Gln
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30 Phe Asn Pro Arg Asp Val Glu Gly Tyr Arg Gln Phe Leu Asp Tyr Ser
 115 120 125

35 Arg Ala Val Phe Lys Glu Gly Tyr Leu Lys Leu Gly Thr Val Pro Phe
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40 Leu Ser Phe Arg Asp Met Leu Arg Ala Ala Pro Gln Leu Ala Lys Leu
 145 150 155 160

45 Gln Ala Trp Arg Ser Val Tyr Ser Lys Val Ala Ser Tyr Ile Glu Asp
 165 170 175

50 Glu His Leu Arg Gln Ala Phe Ser Phe His Ser Leu Leu Val Gly Gly
 180 185 190

55 Asn Pro Phe Ala Thr Ser Ser Ile Tyr Thr Leu Ile His Ala Leu Glu
 195 200 205

Arg Glu Trp Gly Val Trp Phe Pro Arg Gly Gly Thr Gly Ala Leu Val
 210 215 220
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Gln Gly Met Ile Lys Leu Phe Gln Asp Leu Gly Gly Glu Val Val Leu
 225 230 235 240

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Asn Ala Arg Val Ser His Met Glu Thr Thr Gly Asn Lys Ile Glu Ala
 245 250 255

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Val His Leu Glu Asp Gly Arg Arg Phe Leu Thr Gln Ala Val Ala Ser
 260 265 270

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Asn Ala Asp Val Val His Thr Tyr Arg Asp Leu Leu Ser Gln His Pro
 275 280 285

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Ala Ala Val Lys Gln Ser Asn Lys Leu Gln Thr Lys Arg Met Ser Asn
 290 295 300

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Ser Leu Phe Val Leu Tyr Phe Gly Leu Asn His His His Asp Gln Leu
 305 310 315 320

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Glu Ile Phe Asn His Asp Gly Leu Ala Glu Asp Phe Ser Leu Tyr Leu
 340 345 350

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His Ala Pro Cys Val Thr Asp Ser Ser Leu Ala Pro Glu Gly Cys Gly
 355 360 365

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Ser Tyr Tyr Val Leu Ala Pro Val Pro His Leu Gly Thr Ala Asn Leu
 370 375 380

Asp Trp Thr Val Glu Gly Pro Lys Leu Arg Asp Arg Ile Phe Ala Tyr
385 390 395 400

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Leu Glu Gln His Tyr Met Pro Gly Leu Arg Ser Gln Leu Val Thr His
405 410 415

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Arg Met Phe Thr Pro Phe Asp Phe Arg Asp Gln Leu Asn Ala Tyr His
420 425 430

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Gly Ser Ala Phe Ser Val Glu Pro Val Leu Thr Gln Ser Ala Trp Phe
435 440 445

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Arg Pro His Asn Arg Asp Lys Thr Ile Thr Asn Leu Tyr Leu Val Gly
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Lys Ala Thr Ala Gly Leu Met Leu Glu Asp Leu Ile
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 Gly Lys Lys Val Lys Met Asn Thr Met Ile Arg Ser Lys Leu Phe Ser
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15 att cgg tgc gct ttg gac act aag gtg tct gat atg agc gtc aat gct 144
 Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala
 35 40 45

20 cca aaa gga ttg ttt cca cca gag cct gag cac tac agg ggg cca aag 192
 Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys
 50 55 60

25 ctt aaa gtg gct atc att gga gct ggg ctc gct ggc atg tca act gca 240
 Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala
 65 70 75 80

gtg gag ctt ttg gat caa ggg cat gag gtt gac ata tat gaa tcc aga 288
 Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
 85 90 95

30 caa ttt att ggt ggt aaa gtc ggt tct ttt gta gat aag cgt gga aac 336
 Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn
 100 105 110

35 cat att gaa atg gga ctc cat gtg ttt ttt ggt tgc tat aac aat ctt 384
 His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu
 115 120 125

40 ttc aga ctt atg aaa aag gta ggt gca gat gaa aat tta ctg gtg aag 432
 Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys
 130 135 140

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 Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu
 145 150 155 160

214

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5	cta aca act aat caa ctg aag cct tat gat aaa gca agg aat gct gtg Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val 180 185 190	576
10	gct ctt gcc ctt agc cca gtt gta cgt gct ctt att gat cca aat ggt Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly 195 200 205	624
15	gca atg cag gat ata agg aac tta gat aat att agc ttt tct gat tgg Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp 210 215 220	672
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	cca gtt gct tat gcc ctc gga ttt att gac tgt gat aat atc agt gcc Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala 245 250 255	768
25	cgt tgt atg ctt act ata ttt tct cta ttt gct act aag aca gaa gct Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala 260 265 270	816
30	tct ctg ttg cgt atg ttg aag ggt tcg cct gat gtt tac tta agc ggt Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly 275 280 285	864
35	cct ata aga aag tat att aca gat aaa ggt gga agg ttt cac cta agg Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg 290 295 300	912
40	tgg ggg tgt aga gag ata ctt tat gat gaa cta tca aat ggc gac aca Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr 305 310 315 320	960
	tat atc aca ggc att gca atg tcg aag gct acc aat aaa aaa ctt gtg Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val 325 330 335	1008
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215

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	355 360 365	
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	370 375 380	
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	385 390 395 400	
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	405 410 415	
25	tgt ttt tct gat ctt gca ctc tcg tcg cct gaa gat tat tat att gaa Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu	1296
	420 425 430	
30	gga caa ggg tcc cta ata cag gct gtt ctc acg cca ggg gat cca tac Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr	1344
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	450 455 460	
40	ttg gat tta ttc cca tcc tct caa ggc ctg gaa gtt cta tgg tct tcg Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser	1440
	465 470 475 480	
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	485 490 495	
50	cca ttc aga cct gat cag aag aca cca gta aaa aat ttc ttc ctt gca Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala	1536
	500 505 510	
55	ggg tca tac acc aaa cag gat tac att gac agt atg gaa gga gcg acc Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr	1584

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	cta tcg ggg aga caa gca gct gca tat atc tgc agc gcc ggt gaa gat			1632
	Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp			
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	ctg gca gca ctt cgc aag aag atc gct gct gat cat cca gag caa ctg			1680
	Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu			
	545	550	555	560
10	atc aac aaa gat tct aac gtg tcg gat gaa ctg agt ctc gta taa			1725
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35	Ile Arg Ser Ala Leu Asp Thr Lys Val Ser Asp Met Ser Val Asn Ala			
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40	Pro Lys Gly Leu Phe Pro Pro Glu Pro Glu His Tyr Arg Gly Pro Lys			
	50	55	60	
45	Leu Lys Val Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ser Thr Ala			
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Val Glu Leu Leu Asp Gln Gly His Glu Val Asp Ile Tyr Glu Ser Arg
 85 90 95
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Gln Phe Ile Gly Gly Lys Val Gly Ser Phe Val Asp Lys Arg Gly Asn
 100 105 110

10 His Ile Glu Met Gly Leu His Val Phe Phe Gly Cys Tyr Asn Asn Leu
 115 120 125

15 Phe Arg Leu Met Lys Lys Val Gly Ala Asp Glu Asn Leu Leu Val Lys
 130 135 140

20 Asp His Thr His Thr Phe Val Asn Arg Gly Gly Glu Ile Gly Glu Leu
 145 150 155 160

Asp Phe Arg Leu Pro Met Gly Ala Pro Leu His Gly Ile Arg Ala Phe
 165 170 175
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Leu Thr Thr Asn Gln Leu Lys Pro Tyr Asp Lys Ala Arg Asn Ala Val
 180 185 190

30 Ala Leu Ala Leu Ser Pro Val Val Arg Ala Leu Ile Asp Pro Asn Gly
 195 200 205

35 Ala Met Gln Asp Ile Arg Asn Leu Asp Asn Ile Ser Phe Ser Asp Trp
 210 215 220

40 Phe Leu Ser Lys Gly Gly Thr Arg Met Ser Ile Gln Arg Met Trp Asp
 225 230 235 240

Pro Val Ala Tyr Ala Leu Gly Phe Ile Asp Cys Asp Asn Ile Ser Ala
 245 250 255
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Arg Cys Met Leu Thr Ile Phe Ser Leu Phe Ala Thr Lys Thr Glu Ala
 260 265 270

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Ser Leu Leu Arg Met Leu Lys Gly Ser Pro Asp Val Tyr Leu Ser Gly
 275 280 285

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Pro Ile Arg Lys Tyr Ile Thr Asp Lys Gly Gly Arg Phe His Leu Arg
 290 295 300

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Trp Gly Cys Arg Glu Ile Leu Tyr Asp Glu Leu Ser Asn Gly Asp Thr
 305 310 315 320

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Tyr Ile Thr Gly Ile Ala Met Ser Lys Ala Thr Asn Lys Lys Leu Val
 325 330 335

Lys Ala Asp Val Tyr Val Ala Ala Cys Asp Val Pro Gly Ile Lys Arg
 340 345 350

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Leu Ile Pro Ser Glu Trp Arg Glu Trp Asp Leu Phe Asp Asn Ile Tyr
 355 360 365

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Lys Leu Val Gly Val Pro Val Val Thr Val Gln Leu Arg Tyr Asn Gly
 370 375 380

35

Trp Val Thr Glu Met Gln Asp Leu Glu Lys Ser Arg Gln Leu Arg Ala
 385 390 395 400

40

Ala Val Gly Leu Asp Asn Leu Leu Tyr Thr Pro Asp Ala Asp Phe Ser
 405 410 415

Cys Phe Ser Asp Leu Ala Leu Ser Ser Pro Glu Asp Tyr Tyr Ile Glu
 420 425 430

45

219

Gly Gln Gly Ser Leu Ile Gln Ala Val Leu Thr Pro Gly Asp Pro Tyr
 435 440 445

5 Met Pro Leu Pro Asn Asp Ala Ile Ile Glu Arg Val Arg Lys Gln Val
 450 455 460

10 Leu Asp Leu Phe Pro Ser Ser Gln Gly Leu Glu Val Leu Trp Ser Ser
 465 470 475 480

15 Val Val Lys Ile Gly Gln Ser Leu Tyr Arg Glu Gly Pro Gly Lys Asp
 485 490 495

Pro Phe Arg Pro Asp Gln Lys Thr Pro Val Lys Asn Phe Phe Leu Ala
 500 505 510

20 Gly Ser Tyr Thr Lys Gln Asp Tyr Ile Asp Ser Met Glu Gly Ala Thr
 515 520 525

25 Leu Ser Gly Arg Gln Ala Ala Ala Tyr Ile Cys Ser Ala Gly Glu Asp
 530 535 540

30 Leu Ala Ala Leu Arg Lys Lys Ile Ala Ala Asp His Pro Glu Gln Leu
 545 550 555 560

Ile Asn Lys Asp Ser Asn Val Ser Asp Glu Leu Ser Leu Val
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<211> 1848

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<212> DNA

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<220>

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<222> (1)..(1848)

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20 tgc aag act gta gct ttg ggt gat agc aaa cca aga tac aat aaa cag 96
 Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
 20 25 30

25 aga agt tct tgt ttt gac cct ttg ata att gga aat tgt act gat cag 144
 Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 35 40 45

cag cag ctt tgt ggc ttg agt tgg ggg gtg gac aag gct aag gga aga 192
 Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
 50 55 60

30 aga ggg ggt act gtt tcc aat ttg aaa gca gtt gta gat gta gac aaa 240
 Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

35 aga gtg gag agc tat ggc agt agt gat gta gaa gga aat gag agt ggc 288
 Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

40 agc tat gat gcc att gtt ata ggt tca gga ata ggt gga ttg gtg gca 336
 Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

gcg acg cag ctg gcg gtt aag gga gct aag gtt tta gtt ctg gag aag 384
 Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 115 120 125

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221

	tat gtt att cct ggt gga agc tct ggc ttt tac gag agg gat ggt tat	432
	Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr	
	130 135 140	
5	aag ttt gat gtt ggt tca tca gtg atg ttt gga ttc agt gat aag gga	480
	Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly	
	145 150 155 160	
10	aac ctc aat tta att act caa gca ttg gca gca gta gga cgt aaa tta	528
	Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu	
	165 170 175	
15	gaa gtt ata cct gac cca aca act gta cat ttc cac ctg cca aat gac	576
	Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp	
	180 185 190	
20	ctt tct gtt cgt ata cac cga gag tat gat gac ttc att gaa gag ctt	624
	Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu	
	195 200 205	
	gtg agt aaa ttt cca cat gaa aag gaa ggg att atc aaa ttt tac agt	672
	Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser	
	210 215 220	
25	gaa tgc tgg aag atc ttt aat tct ctg aat tca ttg gaa ctg aag tct	720
	Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser	
	225 230 235 240	
30	ttg gag gaa ccc atc tac ctt ttt ggc cag ttc ttt aag aag ccc ctt	768
	Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu	
	245 250 255	
35	gaa tgc ttg act ctt gcc tac tat ttg ccc cag aat gct ggt agc atc	816
	Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile	
	260 265 270	
40	gct cgg aag tat ata aga gat cct ggg ttg ctg tct ttt ata gat gca	864
	Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala	
	275 280 285	
	gag tgc ttt atc gtg agt aca gtt aat gca tta caa aca cca atg atc	912
	Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile	
	290 295 300	
45	aat gca agc atg gtt cta tgt gac aga cat ttt ggc gga atc aac tac	960

222

[illegible]

223

	485	490	495	
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	Arg Ile Ile Ser Arg Leu Glu Lys Thr Leu Phe Pro Gly Leu Lys Ser			
5	500	505	510	
	tct att ctc ttt aag gag gtg gga act cca aag acc cac aga cga tac	1584		
	Ser Ile Leu Phe Lys Glu Val Gly Thr Pro Lys Thr His Arg Arg Tyr			
	515	520	525	
10				
	ctt gct cgt gat agt ggt acc tat gga cca atg cca cgc gga aca cct	1632		
	Leu Ala Arg Asp Ser Gly Thr Tyr Gly Pro Met Pro Arg Gly Thr Pro			
	530	535	540	
15				
	aag gga ctc ctg gga atg cct ttc aat acc act gct ata gat ggt cta	1680		
	Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu			
	545	550	555	560
	tat tgt gtt ggc gat agt tgc ttc cca gga caa ggt gtt ata gct gta	1728		
20	Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val			
	565	570	575	
	gcc ttt tca gga gta atg tgc gct cat cgt gtt gca gct gac tta ggg	1776		
	Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly			
25	580	585	590	
	ttt gaa aaa aaa tca gat gtg ctg gac agt gct ctt ctt aga cta ctt	1824		
	Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu			
	595	600	605	
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	ggt tgg tta agg aca cta gca tga	1848		
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<400> 134

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Cys Lys Thr Val Ala Leu Gly Asp Ser Lys Pro Arg Tyr Asn Lys Gln
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Arg Ser Ser Cys Phe Asp Pro Leu Ile Ile Gly Asn Cys Thr Asp Gln
 35 40 45

15

Gln Gln Leu Cys Gly Leu Ser Trp Gly Val Asp Lys Ala Lys Gly Arg
 50 55 60

20

Arg Gly Gly Thr Val Ser Asn Leu Lys Ala Val Val Asp Val Asp Lys
 65 70 75 80

Arg Val Glu Ser Tyr Gly Ser Ser Asp Val Glu Gly Asn Glu Ser Gly
 85 90 95

25

Ser Tyr Asp Ala Ile Val Ile Gly Ser Gly Ile Gly Gly Leu Val Ala
 100 105 110

30

Ala Thr Gln Leu Ala Val Lys Gly Ala Lys Val Leu Val Leu Glu Lys
 115 120 125

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Tyr Val Ile Pro Gly Gly Ser Ser Gly Phe Tyr Glu Arg Asp Gly Tyr
 130 135 140

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Lys Phe Asp Val Gly Ser Ser Val Met Phe Gly Phe Ser Asp Lys Gly
 145 150 155 160

Asn Leu Asn Leu Ile Thr Gln Ala Leu Ala Ala Val Gly Arg Lys Leu
 165 170 175

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225

Glu Val Ile Pro Asp Pro Thr Thr Val His Phe His Leu Pro Asn Asp
 180 185 190

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Leu Ser Val Arg Ile His Arg Glu Tyr Asp Asp Phe Ile Glu Glu Leu
 195 200 205

10

Val Ser Lys Phe Pro His Glu Lys Glu Gly Ile Ile Lys Phe Tyr Ser
 210 215 220

15

Glu Cys Trp Lys Ile Phe Asn Ser Leu Asn Ser Leu Glu Leu Lys Ser
 225 230 235 240

20

Leu Glu Glu Pro Ile Tyr Leu Phe Gly Gln Phe Phe Lys Lys Pro Leu
 245 250 255

Glu Cys Leu Thr Leu Ala Tyr Tyr Leu Pro Gln Asn Ala Gly Ser Ile
 260 265 270

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Ala Arg Lys Tyr Ile Arg Asp Pro Gly Leu Leu Ser Phe Ile Asp Ala
 275 280 285

30

Glu Cys Phe Ile Val Ser Thr Val Asn Ala Leu Gln Thr Pro Met Ile
 290 295 300

35

Asn Ala Ser Met Val Leu Cys Asp Arg His Phe Gly Gly Ile Asn Tyr
 305 310 315 320

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Pro Val Gly Gly Val Gly Glu Ile Ala Lys Ser Leu Ala Lys Gly Leu
 325 330 335

Asp Asp His Gly Ser Gln Ile Leu Tyr Arg Ala Asn Val Thr Ser Ile
 340 345 350

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226

	Ile	Leu	Asp	Asn	Gly	Lys	Ala	Val	Gly	Val	Lys	Leu	Ser	Asp	Gly	Arg
		355						360						365		
5	Lys	Phe	Tyr	Ala	Lys	Thr	Ile	Val	Ser	Asn	Ala	Thr	Arg	Trp	Asp	Thr
		370					375					380				
10	Phe	Gly	Lys	Leu	Leu	Lys	Ala	Glu	Asn	Leu	Pro	Lys	Glu	Glu	Glu	Asn
	385					390					395					400
15	Phe	Gln	Lys	Ala	Tyr	Val	Lys	Ala	Pro	Ser	Phe	Leu	Ser	Ile	His	Met
				405					410						415	
20	Gly	Val	Lys	Ala	Asp	Val	Leu	Pro	Pro	Asp	Thr	Asp	Cys	His	His	Phe
				420					425					430		
25	Val	Leu	Glu	Asp	Asp	Trp	Thr	Asn	Leu	Glu	Lys	Pro	Tyr	Gly	Ser	Ile
		435						440						445		
30	Phe	Leu	Ser	Ile	Pro	Thr	Val	Leu	Asp	Ser	Ser	Leu	Ala	Pro	Glu	Gly
		450						455					460			
35	His	His	Ile	Leu	His	Ile	Phe	Thr	Thr	Ser	Ser	Ile	Glu	Asp	Trp	Glu
	465					470				475						480
40	Gly	Leu	Ser	Pro	Lys	Asp	Tyr	Glu	Ala	Lys	Lys	Glu	Val	Val	Ala	Glu
					485					490					495	
45	Arg	Ile	Ile	Ser	Arg	Leu	Glu	Lys	Thr	Leu	Phe	Pro	Gly	Leu	Lys	Ser
				500					505					510		
50	Ser	Ile	Leu	Phe	Lys	Glu	Val	Gly	Thr	Pro	Lys	Thr	His	Arg	Arg	Tyr
		515						520					525			
55	Leu	Ala	Arg	Asp	Ser	Gly	Thr	Tyr	Gly	Pro	Met	Pro	Arg	Gly	Thr	Pro

227

530

535

540

5 Lys Gly Leu Leu Gly Met Pro Phe Asn Thr Thr Ala Ile Asp Gly Leu
 545 550 555 560

10 Tyr Cys Val Gly Asp Ser Cys Phe Pro Gly Gln Gly Val Ile Ala Val
 565 570 575

15 Ala Phe Ser Gly Val Met Cys Ala His Arg Val Ala Ala Asp Leu Gly
 580 585 590

Phe Glu Lys Lys Ser Asp Val Leu Asp Ser Ala Leu Leu Arg Leu Leu
 595 600 605

20 Gly Trp Leu Arg Thr Leu Ala
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25 <210> 135

<211> 1233

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30 <213> Tagetes erecta

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<222> (1)..(1233)

40 <223>

<400> 135

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48

228

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	1				5					10					15		
	tct	tct	tca	atc	tct	act	ggc	tgt	tca	ctc	tcc	ccc	ttc	ttc	ctc	aaa	96
5	Ser	Ser	Ser	Ile	Ser	Thr	Gly	Cys	Ser	Leu	Ser	Pro	Phe	Phe	Leu	Lys	
					20				25					30			
	tca	tct	tct	cat	tcc	cct	aac	cct	cgc	cga	cac	cgc	cgc	tcc	gcc	gta	144
10	Ser	Ser	Ser	His	Ser	Pro	Asn	Pro	Arg	Arg	His	Arg	Arg	Ser	Ala	Val	
				35				40					45				
	tgc	tgc	tct	ttc	gcc	tca	ctc	gac	tct	gca	aaa	atc	aaa	gtc	gtt	ggc	192
	Cys	Cys	Ser	Phe	Ala	Ser	Leu	Asp	Ser	Ala	Lys	Ile	Lys	Val	Val	Gly	
		50					55				60						
15	gtc	ggg	ggg	ggg	ggc	aac	aat	gcc	gtt	aac	cgc	atg	att	ggg	agc	ggc	240
	Val	Gly	Gly	Gly	Gly	Asn	Asn	Ala	Val	Asn	Arg	Met	Ile	Gly	Ser	Gly	
	65					70				75					80		
20	tta	cag	ggg	gtt	gat	ttt	tac	gcc	att	aac	acg	gac	tca	caa	gcg	ctt	288
	Leu	Gln	Gly	Val	Asp	Phe	Tyr	Ala	Ile	Asn	Thr	Asp	Ser	Gln	Ala	Leu	
					85				90					95			
	ctg	caa	tct	gtt	gca	cat	aac	cct	att	caa	att	ggg	gag	ctt	ttg	act	336
25	Leu	Gln	Ser	Val	Ala	His	Asn	Pro	Ile	Gln	Ile	Gly	Glu	Leu	Leu	Thr	
				100				105					110				
	cgt	gga	tta	ggg	act	ggg	ggg	aac	ccg	ctt	ttg	gga	gaa	cag	gct	gcg	384
	Arg	Gly	Leu	Gly	Thr	Gly	Gly	Asn	Pro	Leu	Leu	Gly	Glu	Gln	Ala	Ala	
30			115				120				125						
	gag	gag	tcg	aag	gaa	gcg	att	ggg	aat	gcg	ctt	aaa	ggg	tcg	gat	ctt	432
	Glu	Glu	Ser	Lys	Glu	Ala	Ile	Gly	Asn	Ala	Leu	Lys	Gly	Ser	Asp	Leu	
		130				135				140							
35	gtg	ttt	ata	aca	gca	ggg	atg	ggg	ggg	ggg	acg	ggg	tcg	ggg	gct	gct	480
	Val	Phe	Ile	Thr	Ala	Gly	Met	Gly	Gly	Gly	Thr	Gly	Ser	Gly	Ala	Ala	
	145				150			155					160				
40	cca	gtt	gta	gcg	cag	ata	gcg	aaa	gaa	gca	ggg	tat	tta	act	gtt	ggg	528
	Pro	Val	Val	Ala	Gln	Ile	Ala	Lys	Glu	Ala	Gly	Tyr	Leu	Thr	Val	Gly	
					165			170					175				
	gtt	gta	acg	tac	cca	ttc	agc	ttt	gaa	ggc	cgt	aaa	aga	tca	gta	cag	576
45	Val	Val	Thr	Tyr	Pro	Phe	Ser	Phe	Glu	Gly	Arg	Lys	Arg	Ser	Val	Gln	

	180	185	190	
	gcg tta gag gct att gag aag ctg caa aag aac gtt gac aca ctt ata			624
	Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val Asp Thr Leu Ile			
5	195	200	205	
	gtg att cca aat gac cgt ttg ctg gat att gct gat gaa aac acg cct			672
	Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro			
	210	215	220	
10				
	ctt cag gat gct ttt ctt ctt gct gat gat gta ctc cgc caa gga gtt			720
	Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val			
	225	230	235	240
	caa gga atc tca gat ata att aca ata cct ggg ctg gta aat gtg gac			768
15	Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp			
	245	250	255	
	ttt gca gac gtt aaa gca gtc atg aaa gat tct gga act gca atg ctt			816
20	Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu			
	260	265	270	
	ggg gtc ggt gtt tcc tca agt aaa aac cga gct gaa gaa gca gct gaa			864
	Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu			
25	275	280	285	
	caa gca act ctt gct cct ttg att gga tca tca att caa tct gct aca			912
	Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr			
	290	295	300	
30				
	ggg gtt gtt tat aat att acc gga ggg aag gac ata act cta caa gaa			960
	Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu			
	305	310	315	320
	gtc aac agg gtt tct cag gtg gta aca agt ttg gca gat cca tca gca			1008
35	Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala			
	325	330	335	
	aac att ata ttc ggg gca gtg gta gat gag aga tac aac ggg gag att			1056
40	Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile			
	340	345	350	
	cat gtg acc att gtt gct act ggc ttt gcc cag tcg ttt cag aaa tct			1104
	His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser			
45	355	360	365	

ctt ctt gct gac ccg aaa gga gca aaa ctt gtt gat aga aat caa gaa 1152
 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

5 cct aca caa cct ttg act tcc gcg aga tct ttg aca aca cct tct ect 1200
 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

10 gct ccg tct ccg tct agg aaa ctc ttc ttt taa 1233
 Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
 405 410

15 <210> 136
 <211> 410
 <212> PRT

20 <213> Tagetes erecta

25 <400> 136
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 20 25 30

35 Ser Ser Ser His Ser Pro Asn Pro Arg Arg His Arg Arg Ser Ala Val
 35 40 45

40 Cys Cys Ser Phe Ala Ser Leu Asp Ser Ala Lys Ile Lys Val Val Gly
 50 55 60

45 Val Gly Gly Gly Gly Asn Asn Ala Val Asn Arg Met Ile Gly Ser Gly
 65 70 75 80

231

Leu Gln Gly. Val Asp Phe Tyr Ala Ile Ash Thr Asp Ser Gln Ala Leu
85 90 95

5

Leu Gln Ser Val Ala His Asn Pro Ile Gln Ile Gly Glu Leu Leu Thr
100 105 110

10 Arg Gly Leu Gly Thr Gly Gly Asn Pro Leu Leu Gly Glu Gln Ala Ala
115 120 125

Glu Glu Ser Lys Glu Ala Ile Gly Asn Ala Leu Lys Gly Ser Asp Leu
15 130 135 140

Val Phe Ile Thr Ala Gly Met Gly Gly Gly Thr Gly Ser Gly Ala Ala
145 150 155 160

Pro Val Val Ala Gln Ile Ala Lys Glu Ala Gly Tyr Leu Thr Val Gly
165 170 175

25

Val Val Thr Tyr Pro Phe Ser Phe Glu Gly Arg Lys Arg Ser Val Gln
180 185 190

30 Ala Leu Glu Ala Ile Glu Lys Leu Gln Lys Asn Val. Asp Thr Leu Ile
195 200 205

Val Ile Pro Asn Asp Arg Leu Leu Asp Ile Ala Asp Glu Asn Thr Pro
35 210 215 220

Leu Gln Asp Ala Phe Leu Leu Ala Asp Asp Val Leu Arg Gln Gly Val
225 230 235 240

Gln Gly Ile Ser Asp Ile Ile Thr Ile Pro Gly Leu Val Asn Val Asp
245 250 255

45

232

Phe Ala Asp Val Lys Ala Val Met Lys Asp Ser Gly Thr Ala Met Leu
 260 265 270

5 Gly Val Gly Val Ser Ser Ser Lys Asn Arg Ala Glu Glu Ala Ala Glu
 275 280 285

10 Gln Ala Thr Leu Ala Pro Leu Ile Gly Ser Ser Ile Gln Ser Ala Thr
 290 295 300

15 Gly Val Val Tyr Asn Ile Thr Gly Gly Lys Asp Ile Thr Leu Gln Glu
 305 310 315 320

Val Asn Arg Val Ser Gln Val Val Thr Ser Leu Ala Asp Pro Ser Ala
 325 330 335

20 Asn Ile Ile Phe Gly Ala Val Val Asp Glu Arg Tyr Asn Gly Glu Ile
 340 345 350

25 His Val Thr Ile Val Ala Thr Gly Phe Ala Gln Ser Phe Gln Lys Ser
 355 360 365

30 Leu Leu Ala Asp Pro Lys Gly Ala Lys Leu Val Asp Arg Asn Gln Glu
 370 375 380

35 Pro Thr Gln Pro Leu Thr Ser Ala Arg Ser Leu Thr Thr Pro Ser Pro
 385 390 395 400

Ala Pro Ser Arg Ser Arg Lys Leu Phe Phe
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<211> 891

<212> DNA

<213> Tagetes erecta

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<220>

<221> CDS

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<222> (1)..(891)

<223>

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<400> 137

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act ttc ccc aca ttc aat ccc cta cac aaa acc cta act aaa cca aca 96
 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
 20 25 30

cca aaa ccc tac cca aag cca cca cca att cgc tcc gtc ctt caa tac 144
 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
 35 40 45

aat cgc aaa cca gag ctc gcc gga gac act cca cga gtc gtc gca atc 192
 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60

gac gcc gac gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa 240
 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

aac cgc gtc aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga 288
 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 40 85 90 95

ctc gac caa gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg 336
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110

45

234

	ctt tgt att tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga	384
	Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly	
	115 120 125	
5	aaa gct tta gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc	432
	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys	
	130 135 140	
10	ccg gat ttt ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc	480
	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe	
	145 150 155 160	
15	ata acc gcc att aca ccg gct aac gaa gcc gta tta gtt aca aca cct	528
	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro	
	165 170 175	
20	gat att act gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa	576
	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu	
	180 185 190	
	tgt gat gga att agg gat att aaa atg att gtg aac aga gtt aga act	624
	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr	
	195 200 205	
25	gat ttg ata agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag	672
	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu	
	210 215 220	
30	atg ttg gga ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att	720
	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile	
	225 230 235 240	
35	cgg agt acg aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act	768
	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr	
	245 250 255	
40	tta gca gga ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa	816
	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln	
	260 265 270	
	gat agc atg aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga	864
	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly	
	275 280 285	
45	ttt ttc tcg ttt ttt gga ggt tag tga	891

Phe Phe Ser Phe Phe Gly Gly
 290 295

5 <210> 138

<211> 295

<212> PRT

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<213> Tagetes erecta

15 <400> 138

Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser
 1 5 10 15

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Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr
 20 25 30

25

Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr
 35 40 45

30

Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile
 50 55 60

35

Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu
 65 70 75 80

Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg
 85 90 95

40

Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu
 100 105 110

45

Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly

236

	115	120	125
5	Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys		
	130	135	140
10	Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe		
	145	150	155 160
	Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro		
	165	170	175
15	Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu		
	180	185	190
20	Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr		
	195	200	205
25	Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu		
	210	215	220
30	Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile		
	225	230	235 240
	Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr		
	245	250	255
35	Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln		
	260	265	270
40	Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly		
	275	280	285
45	Phe Phe Ser Phe Phe Gly Gly		
	290	295	

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5 <211> 332

<212> DNA

<213> Tagetes erecta

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15 <221> CDS

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<400> 139

25 aag ctt gca cga gcc tct ctc tat ttt tac act tca atg gcg gca gca 48
 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

30 att gct gtc cct tgt agc tca aga cca ttt ggc tta ggt cga atg cgg 96
 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

35 tta ctt ggt cat aaa ccc aca acc ata act tgt cac ttc ccc ttt tct 144
 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

40 ttt tct atc aaa tca ttt acc cca att gtt agg ggc aga aga tgt act 192
 Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

40 gtt tgt ttt gtt gcc ggt ggc gac agt aat agt aac agt aat aat aat 240
 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

45 agt gac agt aat agt aat aat ccg ggt ctg gat tta aac ccg gcg gtt 288
 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val

238

85

90

95

atg aac cgt aac cgt ttg gtt gaa gaa aaa atg gag agg tcg ac
 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser

332

5 100 105 110

<210> 140

10 <211> 110

<212> PRT

<213> Tagetes erecta

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<400> 140

20 Lys Leu Ala Arg Ala Ser Leu Tyr Phe Tyr Thr Ser Met Ala Ala Ala
 1 5 10 15

25 Ile Ala Val Pro Cys Ser Ser Arg Pro Phe Gly Leu Gly Arg Met Arg
 20 25 30

30 Leu Leu Gly His Lys Pro Thr Thr Ile Thr Cys His Phe Pro Phe Ser
 35 40 45

Phe Ser Ile Lys Ser Phe Thr Pro Ile Val Arg Gly Arg Arg Cys Thr
 50 55 60

35 Val Cys Phe Val Ala Gly Gly Asp Ser Asn Ser Asn Ser Asn Asn Asn
 65 70 75 80

40 Ser Asp Ser Asn Ser Asn Asn Pro Gly Leu Asp Leu Asn Pro Ala Val
 85 90 95

45 Met Asn Arg Asn Arg Leu Val Glu Glu Lys Met Glu Arg Ser
 100 105 110

<210> 141

5 <211> 332

<212> DNA

10 <213> Tagetes erceta

<220>

15 <221> misc_feature

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20 <223> β -Hydroxylase Sense Fragment

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tgtagctcaa gaccatttgg cttaggtcga atgcggttac ttggtcataa acccacaacc 120

ataacttgtc acttcccctt ttctttttct atcaaatcat ttaccccaat tgtagggggc 180

30 agaagatgta ctgtttgttt tgttgccggt ggcgacagta atagtaacag taataataat 240

agtgacagta atagtaataa tccgggtctg gatttaaacc cggcggttat gaaccgtaac 300

cgtttggttg aagaaaaaat ggagaggtcg ac 332

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<210> 142

<211> 332

40 <212> DNA

<213> Tagetes erecta

<220>

5 <221> misc_feature

<222> (1)..(332)

<223> β -Hydroxylase Antisense Fragment

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<400> 142

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gaattcggca cgagcctctc tctattttta cacttcaatg gcggcagcaa ttgctgtccc 60

ttgtagctca agaccatttg gcttaggtcg aatgcggtta cttggtcata aaccacaac 120

cataacttgt cacttccctt tttctttttc tatcaaatac tttaccccaa ttgttagggg 180

20

cagaagatgt actgtttggt ttgttgccgg tggcgacagt aatagtaaca gtaataataa 240

tagtgacagt aatagtaata atccgggtct ggatttaaac ccggcggtta tgaaccgtaa 300

ccgttttggtt gaagaaaaaa tggagaggat cc 332

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